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GenCore version 5.1.6
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September 7, 2004, 19:46:08; Search time 26569 Seconds (without alignments) 7119.161 Million cell updates/sec - nucleic search, using sw model OM nucleic Run on:

Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3470272 segs, 21671516995 residues Searched:

6940544 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

GenEmbl:\* Database :

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	14	2431.2		55		AX877347	AX877347 Sequence
	12	2431.2		55		BD156611	BD156611 Primer fo
O	16	2080		16		AL589649	ALS89649 Human DNA
	17	1729.4		50		AX877018	AX877018 Sequence
	18	1729.4		59		BD156441	BD156441 Primer fo
	13	1729.4		50		AK001570	AK001570 Homo sapi
	50	1191.2		79		AX834513	AX834513 Sequence
	21	1191.2		79		AK097021	AK097021 Homo sapi
	22	790.2		41		AX776296	AX776296 Sequence
	23	788.6		41		AX776298	AX776298 Sequence
	24	788.6		43		AX776294	AX776294 Sequence
	25	777.6		6		AX776292	Segue
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ALIGNMENTS

авозэлБЭ Rattus norvegicus mRNA for filamin-interacting protein L-FILIP, complete cds. Rattus norvegicus (Norway rat) Sattus norvegicus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; AB055759 AB055759.1 GI:21392398 Rattus. RESULT 1 AB055759 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

Nagano, T., Yoneda, T., Hatanaka, Y., Kubota, C., Murakami, F. and

REFERENCE AUTHORS

us-10-788-793-1.rge

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241 GGCACCTCAAACCATCTGGAGAAAGTGAGAAAAAGACTAAGAAGTTATCCA
                                        301 AGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGGGGTTGCAGGAGGAAGAAGATG
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                                                                                                           Submitted (13-FEB-2001) Makoto Sato, Fukui Medical University, Dept. of Anatomy 2, Faculty of Medicine; 23-3, Shimoalzuki, Matsuoka, Pukui 910-1193, Japan (E-mail:makosatco@fmsrsa.fukui-med.ac.jp, Tel:81-776-61-8305, Fax:81-776-61-8155)
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               Filamin A-interacting protein (FILIP) regulates cortical cell migration out of the ventricular zone Nat. Cell Biol. 4 (7), 495-501 (2002) 22100428
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2 (bases 1 to 4364)
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Direct Submission
Submitted (13-FEB-2001)
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2516 GGAGGAGACCCCGGCTGTGTTCATTCGCAAATCCTTCCAGGAGAAAATCACATCAT 2575 					CTGAAGAGTT           CTGAAGAATT	2876 ITTCTCTAGTACCACCGTCATTCCTACGTAGGAACCAGAACCAGAATAACCATTAT 2935 	2936 TCCATCACCCAATGTCATGTCGCAAAAGCCCAAAAGTGCAGATCCTACGGCCCAGA 2995 	33		3116 TGCAGCTCCCACTGAAATCGCTGTCTCTCTGAATCTCAGGAAGTGCCTATGGGAAGGAC 3175 	AGTACAACTC	n n	3296 TAAQCGATCTCGGGCCTGCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGT 3355		3416 CCTCTCTAAGACCCGGTGCTAGCAAGTGACCAGCACTATAACTATAACCCCGGTCAC 3475 	3476 AACGTCATCCACACGAGGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCC 3535	3536 TACCCCCACCGCATTCCTATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGC 3595 

1495 1615 1675 2155 1757 1315 1375 1937 1435 2057 1555 2177 2237 1735 2297 1795 2357 2417 1915 2477 1975 2035 2597 <u> adaggaagaactrcaagaattaagagataaaattgccaaaggagaatgtggaaactctag</u> GGAGATCACTAAAACTGAATCCCAGTGTAGGGAATTGAGGAAGAAGCTGCAAGAGGAAGA GGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTGAA TCTGGAGAAAGAAAAGAAACTTAACCAAAGACCTGCTAAATGAATTGGAGGTGGTCAAGAG TCGAGTIAAAGAACTCGAATGCTCCGAGAGTAGACTGCAGAAAGGCCGAGTTAAGCCTCAA ACTAAAGAAGAGACTTGATGGTATAGAGGAAGTGGAAAGGAGAAATAACAAGAGGAAGGTC GTGCAAGGGGTCTGAGTTCACCTGCCGGAAGACAATAAGATCAGAGAACTAACGCTTGA AATCGAGAGACTGAAGAACGGCTCCAGCAGTTGGAGGTGGTGGTGGAGGGGGACTTGATGAA AATTGAGAGACTGAAGAAACGTCTCCAACAATTGGAAGTGGTCGAAGGGGGATTTGATGAA GGTTGGCTTAACCCAAAGAATCGAGGAGCTAGAAGAGACCAACAAAAATCTGCAGAAGGC <u>AGAGGAAGAGCTCCAGGAGCTGAGAGAGAGAAATTGCCAAAGGGGAATGTGGAAACTCCAG</u> TCTCATGGCGGAAGTGGAGGTCTGCGCAAGCGCGTGCTTGAGATGGAGGGCAAGGATGA **AGAGATCACGAAGACCGAGGCCCAGTGCCGGGAGCTGAAGAAGAAGCTCCAAGAGGAAGA** ACACCACAGGAAGTTAGACTTAGAAGTGGAGAAGCTGCAGAAGAGGATGTCTGAGCT CCTGGAGAAGGAGAACCTAACCAAAGACCTGCTGAACAGAGGTGGTCGAGGAG rccacitiaaacaarriccaarcriccaaacracarriccaaaaccrcaarraaccrraaa <u> AGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGGGAAAATAT</u> <u> AGATGATCTTACCAAGTTGAAGTCATTTACCGTGATGCTGGTTGATGAAAGGAAAATAT</u> GATGGAGAAAATAAAGCAAGAAGAGGAAAGTGGATGGGTTGAATAAAAACTTTAAGGT GGAGCAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTT GGAACAAGGAAAAGTTATGGATGTAACTGAAAAACTAATTGAAGAAAAGTAAGAAACTTTT AAAACTCAAATCTGAAATGGAGGAAAAAGGAGTACAGTCTGACAAAGGAGGGGATGAGCT GATGGGTAAACTGAGGAGCGAAGAAGAAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTT GACAGAAGATGAGTATGATCAGCTGGAACAGAAATTTAGAACTGAGCAGGATAAGGCTAA CTTCCTCTCCCAGCAGCTCGAGGAAATCAAACGCAAATGGCCAAGCAAAGCCATAGA GACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACCGAGCAGGATAAGGCAAA

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Published Only in Database (2003)
2 (bases 1 to 4247)
Sato,M. and Nagano,T.
Direct Submission
Submitted (31-MAY-2002) Makoto Sato, Fukui Medical University,
Department of Anatomy, Shimoaizuki 23, Matsuoka, Fukui 910-1193,
Japan (E-mail:makosato@fmsrsa.iukui-med.ac.jp,
Tel:81-776-61-8305(exz.2205), Fax:81-776-61-8155)
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/protein_id="BAC77067.1"
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norvegicus

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3426 AGACCCGGTGCTAGCAAAGTGACCAGCACTATAACTATAACCTGGTCACAAGGTCATCC 3485 	3421 GCTCGAGGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCCTACCCCCACC 3545 3421 GCTCGAGGAACCCAGTGAGACAGACAGGTCATCCCAGCGGCCTACACCACC 3480	3546 CGCATTCCTATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCA 3605 	3606 GGAAATCTGACCAAATTCCAGCCTCGAGCTGAGACTCAGTCTATGAAAATAGAGCTGAAG 3665 	3666 AAATCTGCAGCAGCAGCACCATCTCTTGGAGGGGGAAGGGCTGAGGGCAGTGGCTA 3725 	3726 AGGGGTATGTTGTAAGGATGCTACTGCTGCAGTGGAAACCATCCTCTGTGCCAAC 3785 	3786 CCTTTCCTTGTAC-TACTAATTTAAGTTTTAAATATCTTGTTTATAAAATAACCATTTAA 3844 	3845 TAGCCAIGCACCCCCCCCTCCCATTITGIGCATCGITTCAAIGCAGGGAAIAGAATIAAI 3904 	3905 TAGCAGAATTTCTGTTGCTGAATGTTCTGTTGAAGATGTTGGTCCAGTTCAGTTTTACT 3964 11	3965 TCTAGCATGTGGCCCCATTCAAGGTAGCTCACGAGTTGTGAAGCCCTCAATATCGTCACC 4024 1	4025 GGAGAGATITIGAGGACCACATIACATAIGCTCCCAAAGGCTGGCTCCCAATITICCTAAT 4084	4085 TGTAAGCCAACTTTAATAGACTCAGTTCTGTGAT-TTTTTTTCCAAAAAAAAAA	4144 TGAAATAGGACAGAGTTTAACAGTTGTCATTTTGCACTATCAAGCCATGAGTTTGATATA 4203 	4204 TGGGTTATAAGAAA-AGAATACTTTCAGAGCTATCACAGGGGTCTCTAAACTTTTGGAAAA 4262 	4263 ACAAAAGCCCTAATATGACCTCAGGAAACAATTTGAACATGAAATAAAATGGAAATGAA 4322 	CTGTGG	4242 ATATGG 4247
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HTG 10-MAY-2003

Rattus norvegicus clone CH230-83M15, WORKING DRAFT SEQUENCE. AC130850
AC130850.3 GI:30522010
HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.
Rattus norvegicus (Norway rat)

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 6 AC130850 LOCUS

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Muzny, D. Marzie, Meszker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, L., Alsbrooks, S., Adams, A., Angulano, D., Bandaraniske, D., Barber M., Barnstead, M., Banamed, F., Biara, M., Blair, J., Blair, J., Blair, C., Barrell, K., Calderon, E., Cardens, V., Carter, K., Cardens, V., Carter, K., Cardens, V., Carter, K., Cardens, V., Carter, M., Center, A., Cardens, V., Carter, K., Cardens, V., Carter, K., Cardens, C., Dederich, D., Develand, C., Cher, R., Chen, R., Chen, Y., Chen, R., Chen, Y., Chen, M., Chen, M., Dubland, C., Burrell, K., Duval, B., Eaves, K., Deper, H., Dugan-Rochas, S., Dunn, A., Dublan, K., Duval, B., Eaves, K., Deper, H., Dugan-Rochas, S., Dunn, A., Dublan, K., Duval, B., Eaves, K., Deper, H., Dugan-Rochas, S., Dunn, A., Dublan, K., Duval, B., Eaves, K., Deper, M., Eugen, C., Barnar, R., Ganner, T., Garrer, M., Guevara, M., Gunrar, C., Gent, G., Gerrandez, S., Finley, M., Rlagg, N., Forbes, L., Footer, M., Guevara, M., Gunrar, E., Hadun, M., Hamilton, C., Hamilton, K., Harine, S., Hulk, S., Handlen, S., Hadun, S.L., Hodgen, M., Hamilton, C., Hamilton, K., Harrey, Y., Havlak, P., Hawes, A., Hendergon, M., Hamilton, K., Mayor, M., Martin, K., Mayor, M., Martin, K., Mayor, M., Martin, K., Mayor, M., Martin, K., Martin, M., Martin, K., Wata, K., Martin, M., Martin, K., Wata, K., Martin, M., Savery, G., Storer, J., Storen, L., Wa
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aryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; malia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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* Gee http://www.hgac.bom.tmc.edu/docs/Genbark draft_data.html).

* ONTE: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The corder of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This contig of 227874 bp in length.
                                                                                                                                                      Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center: Conter: Interect information
Center: Project Information
Center project Information
Center project Information
Center clone name: GGBD
Center clone name: CH20-89M15
Mssembly program: Aclas 3.0;
Consensus quality: 218658 bases at least Q40
Consensus quality: 218058 bases at least Q30
Consensus quality: 218058 bases at least Q30
Consensus quality: 218227 bases at least Q30
Consensus quality: 21822848; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGTGGACGAGAGGCAGATGCAGCAACTGGGCCTGCAGAGTCAGAAGTCCAG 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                          236254 bp in length
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                                                                    23625 23634: contig of 236254 bp in lengt.
236355 23634: gap of unknown Length.
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ive 0; Mismatches
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ORIGIN .

NOVEL Genetic markers for leukemias  JOURNAL Patent: WO 03039443-A 3001 15-NAY-2003;  Detucaches Kressforschungzeattrem (DB); Haferlach, Tore Loads and Composition (DB); Haferlach, Tore Composition (DB); Haferl	1027 CCAAAGGACTTCAACAAGGCTTCAAGGTTTTCCAAGAGACAGAGAGGGGGGGG
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us-10-788-793-1.rge

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ACCESSION VERSION VERSION VERSION VERSION VERSION REFERENCE AUTHORS TITLE JOURNAL COMMENT GENERE GOUNCE CDS CDS			POLYA_SICE ORIGIN Query Match
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Best Local Matches 298  Qy 34  Qy 181  Qy 153  Qy 270  Qy 270  Qy 330  Qy 330  Qy 450  Db 601  Qy 6510  Ob 601  Ob 601	Similarity   84.4%;   Pred. No. 0;	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1201   CACANTAGGCAACTTAGACTCAAGCTGGTTAACCCAAAGGATCGAGGGGAACTTAGAAATT   150
6 6 6 6 6 6 6 6 6 6 6 6 6 6	630 AAGCACAAGCACCTGACTACATGAACAAGAGCGACGACTTCACCAACCTGCTGGAGCAG 689  781	· · · · · · · · · · · · · · · · · · · ·	

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Best Local Similarity 94.6
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Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Maldrin,J., Mencus,L., Minova,T., Mangay,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Ragov,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Travers,M., Vassiliev,H., Venkataraman,V.S., Yela,R., Vo,A., Wilson,B., Wu,X., Wassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyassiliev,H., Vonkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyassiliev,H., Vonkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyassiliev,H., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission
Submitted (127-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 27, 2003 this sequence version replaced gi:28195942.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1396-1397)
http://ftp.genome.washington.edu/RM/RepeatMasker:html
                                                                                                                                                                                                                                                                                                                                                                                ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 140000; agarose-fp
Insert size: 138453; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; agarose-fp
Quality coverage: 8.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 511 K 11

Center clone name: 511 K 11

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 136131 bases at least Q30

Consensus quality: 131311 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L21329
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of 17857 bp in length
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of 3311 bp in length
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8152: gap of 100 bp
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contig of 650 bp in length
gap of 100 bp
contig of 1723 bp in length
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of 3540 bp in length
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41354 CTGGTGGATGAGGGGGGGAGATGGAGCAGCTGGGCCTGGGCCTGCAGAGTCAGAAAGTCCAG
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Matches 2659; Conservative
    6809
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77370 CACCTGGGTTCTCAGTTTAAGCGATCTCCCGGGCCTGCAGCAGCGGAAGGCGTGAGTCCA 77311
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MCPherson, J. D. and Waterston, R. H.
Direct Submission
Submitsed (13-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 191609)
MCPherson, J. D. and Waterston, R. H.
Direct Submission
Submitted (12-MAR-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 191609) MRPherson, J.D. and Materston, R.H.
                                                                                                                                          77250 CTTCGCTCTCCCAGGAACCACCTCTTTCAAGACCTGGTGCTAACAAAGTGACCAGCACT
                                    3336 GTTATCACCGTCCGGCCTGTCAACGTGACAGCGAGAAGGAGGTTTCTACAGGCACAGTC
                                                                                                               3396 CTTCGCTCTCCCAGGAACCACCTCTTCAAGACCCGGTGCTAGCAAAGTGACCAGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
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1411: gap of unknown length
3859: contig of 2448 bp in length
3959: gap of unknown length
6808: contig of 2849 bp in length
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ACI40247.1 GI:28475485
HTG; HTGS PHASE1; HTGS_FULLTOP.
Mus musculus (house mouse)
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Sincet Submission

Direct Submission

Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisararu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'- end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                            38775
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3559 bp mRNA linear PRI 01-AUG-2002 Homo sapiens cDNA FLJ14799 fis, clone NT2RP4001351, weakly similar to Human ovarian cancer downregulated myosin heavy chain homolog
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KKLQREEELHGSKDELTGERGCGNSSLEKLEBAFSKOLRKGKSETQLHLNLEKEKNLTKDL
LNELEVVKSRVKELECSESRLEKAELSLKDDLTKLKSFTVMLVDERKNMMEKIKQEER
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                     GTTATCACGGTCCGGCCTGTCAACGTAACAGCCGAGAAGGAGGTTTCTACGGGCACAGTC
                                                                                                                                               CTTCGCTCTCCCAGGAACCACCTCTTCAAGACCCGGTGCTAGCAAGTGACCAGCACT
 CACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCT----GCCGCTGAAGGCGTGAGCCCA
                                                                       GTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAGGAGGTTTCTACAGGCACAGTC
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/clone_lib="NT2RP4"
/note="cloning vector: pME18SFL3-mRNA from NT2 no
precursor cells after 2-weeks retinoic acid (RA)
                                                                                                                                                                                                                                                                                                                                                                                                                                              AK027705.1 GI:14042583
oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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/db_xref="GI:14042584"
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/db_xref="taxon:9606"
/clone="NT2RP4001351"
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PTVRKVNSNANIITTEDNKHIHLGSSQFKRSPGTSGEGVSPVITVRPVNVTAEKEVS
TGTVLRSPRNHLSSPRASKVTSTITITPVTTSSARGTQSVSGQDGSSQRPTFTRIPM
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KRLQQLEVVEGDLMKTEDEYDQLEGKERTEGDKANFLSQQLEEIKHOTAKNKAIEKGE
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AEBERINGKNYN FRKSFORDLTKELEISKS YSALARPSVOKRRWDVPVTSTGVQTDAVSGEA
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MRKRENGPSITQEKGPRTNSSPGHPGEVVLSPRQGQPLHIRVTPDHENSTATLEITSP
KVDGLNKNFKVEQGKVMDVTEKLİEESKKLLKLKSEMEEKVYNLTRERDELIGKLKSE
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1052 1172 1112 1232 1292 1352 1412 1472 1532 1592 992 300 812 872 932 180 240 420 480 540 900 9 720 9 AAATCCAAGAAGACGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACAGGCC TCGAGGTTTCCCAGGAGCAGGAGGAGAGGAGCCAAATTGGCGAATCAGAATCTCAC 241 TCGAGGTTTTCTCAAGAGCATGAAGAGATGAACGCTAAACTGGCTAAATCAAGAGTCTCAC CTCATGTTGGTGGACGACAGAGGCACATGCACATCGAGCAACTGGGGCCTGCAGAGACAGAAA GTCCAGGACCTCACTCAGAAGCTGAGGAGGAGGAAGAAAACTCAAAGCGGGTCACTTAC 301 AATAGGCAACTTAGACTCAAGCTGGCTTGGCTTAACCCAAAGAATCGAGGAGCTAGAAGAG 421 AAAGGAGAATGTGGAAACTCTAGCCTCATGGCAGAAGTGGAAATCTTCGAAAGGGTGTG 1233 CTTGAGATGGAGGCAAGGATGAAGAGATCACGAAGACCGAGGCCCAGTGCCGGGAGCTG 1293 AAGAAGAAGCTCCAAGAGGAAGAACACCACAGCAAGGAACTTAGACTTAGAAGTGGAGAAG CTGCAGAAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCG CTACAGAAGAAGAATGITCIGAACTAGAGAAATTGGAAGAAGCATTTAGCAAGAGTAAATCT GAATGCACCCAGCTCCATCTGAACCTGGAGAAGGAGAAGAACCTAACCAAAGACCTGCTG AACGAGCTGGAGGTGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTG GAAAACGCTAAGCGGCTCAACAACTTCGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCC GAAAATGCTAAACGACTCAATAAACTAAGAGATGAGCTTGTTAAACTCAAATCCTTTGCA **AACCGGCAACTTCGACTCAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAAGAG** ACCAATAAAAGCCTTCAGAAGGCAGAGGAAGAGCTCCAGGAGCTGAGAGAAAATTGCC AAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGCGTG 721 AATGAATTGGAGGTGGTCAAGAGTCGAGTTAAAGAATTGGAATGTTCTGAAAGTAGATTG GAGAAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATG Score 2443.2; DB 9; Length 3559; Pred. No. 0; 0; Mismatches 638; Indels 22; ; 0 56.0%; 81.6%; Conservative Similarity Best Local Simi Matches 2918;

EEKSSELSCSVDLLKKRLDGIEEVEREITRGRSRKGSELTCPEDNKIKELTLEIERLK KRLQQLEVVEGDLMKTEDEYDQLEQKFRTEQDKANFLSQQLEEIKHQIAKNKAIEKGE VYSQEAELRHRFRLEEAKSRDLKAGVOALKEKIHELMWKEDQLSQLQVDYSVLQQRFM EEENKNKNMGQEVLNLTKELELSKRYSRALRPSVNGKRMVDVL"	Query Match 55.7%; Score 2431.2; DB 6; Length 3558;  Best Local Similarity 81.5%; Pred. No. 0;  Matches 2917; Conservative 0; Mismatches 638; Indels 23; Gaps 8;  Qy 753 GAAAACGCTCAACAACATCCAGATGGAGCTTGTGAACTCCTTCGCC 812	Db 1 GAAATGCTAAACAATAAACTAAAAAAAAAAAAAAAAAAA	Qy         873 GTCCAGGACCTCACTCAGAAGCTGAGGAAGAAAAACTCAAAGCGGTCACTTAC 932	OY 993 TCGAGGTTTTCCCAGGAGGAGGATGAACGCCAAATTGGCGAATCAAGAATCTCAC 1052		Db   361 ACCAACAAAATCTGCAGAGGGAAGAAGAACTTCAAGAGATTAAGAGATTAAATTGCC 420   Qy	1233 CTTGAGATGGAGGATGAAGATGATCACGAAGACCGAGGCCCAGTGCCGGGAGCTG	ANGARGANGANCICCANGANGANGANCACANGANGANGANGANGANGANGANGANGANGANGANGANGA	Db 601 CTACAGAAGAATCTCGAACTAGAGAATTGGAAGATTTAGCAAGAGTAAATCT 660  Qy 1413 GAATGCACCAGCTCCAGTCTGAACCTGGAGAAGAAGAACCTAACCAAAGACCTGCTG 1472  Db 661 GAGTGCACCCAGCTACATTAAATCTGGAGAAAAAAAAAA	Qy         1473         AACGAGGTGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTG         1532           D         721         AATGAATTGGAGTCGAGTTAAAGATTGGAATTCTGAAAGTAGATTG         780           OV         1533         GAGAAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGCATGATG         1592		Qy 1653 GGGTTGAATAAAACTTTAAGGTGGAGGGAAAAGTCATGGATGTGACGGAAAGGTA 1712 
	Db 3061 TITAAATATTGTGTTTATAAATAACCAACTAATAACCATTTGTCTTTCCCATTTTGT 3118  QY 3872 GCATCTGTTTCAATGCAGGGAATAGAATTAATTAGCAGAATTTCTGTTTGCTGAATGTT 3931	3175 AGCCAGGCGTGGTTTCTAGTTTTGCTTCTAGCAAGTGGACCCATCAATAGACC 32 3992 CTCACGAGTTGTGAAGCCTCAATATCGTCACGGAGAGATTTGAGGACCACATTACATA 40 13235 CATCTGAGCCTGTTTCTCACACATTAGAGACTCAATA-CACA 32	4052 TGCTCCCAAAGGCTGGCTCCCAATTTCCTAATTGTAAGCCAACTTTAATAGACTCAGT 41	Db 3342 CCACAATAATTTTTATTAAAAAATCCTATTACAAAATAAGACATACTTTAACTATTGT 3401  Qy 4171 CATTTGCACTATCAAGCCATGAGTTTGATATATGGGTTATAAGAAA-AGAATACTTTCA 4229  Db 3402 CATTTGCCTCTTTCACATCATGAATTTGCTTTATGTGCTGGAAAAACATCACATAGCTA 3461	QY 4230 GAGCTATCACAGGGTCTCTAAACTTTTGGAAAAACAAAAGCCCCTAATATGACCTCAGGA 4289		AX877347 AX877347 LOCUS LOCUS DEFINITION Sequence 12252 from Patent EP1074617. ACCESSION AX877347 SPESSION AX877347 AX877347.1 GI:40032083	SOURCE Homo sapiens (human) ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. TITLE Primers for synthesising full-length cDNA and their use JOURNAL Patent: EP 1074617-A 12252 07-FEB-2001; Research Association for Bittechnology (JP)	rce	/note="unnamed protein product"  /codon start=1  /protein_id="CAE89684.1" /db.xref="Gi:40032084.1" /tb.xref="Gi:40032084" /translation="MLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAITSKSKED /kranslation="MLVDERQMHIRQLGLQSQKVQDLTQKLREEEEKLKAITSKSKED NIOKAEFETIORIDMYIAKCHGCONSTINAKLANGENRRQLEKLYGGTGREEEFTNK NIOKAEFETIORIDMYIAKCHGCONSTINAKHANDAIDMYIAKUGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	KLOPEEBHUSKEIRLEVEKUSTANGELEKLERAFSKSKSECTOLHINLEKEKNLITKDL LINELEVVKSRVKELECSESRLEKABLEKDELKLISTKJSTVALVDERKNMMEKIKQEER KVDGLINKNFKVEQGKVMDVTEKLIBESKKLLKLKSEMEEKVYNLITRERDELIGKLKSE

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Patent: JP 2002191363-A 11454 09-JUL-2002;

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/11454
PD 09-JUL-2000
PP 28-JUL-2000
PP 28-JUL-2000
PP 28-JUL-2000
PP 105-MARAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 3558)

                                    CTGTTGAAGATGTTGGTCCAGTTCAGTTTTACTTCTAGCATGTGGCCCCATTCAAGGTAG
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                                                                                   CTCACGAGTTGTGAAGCCCTCAATATCGTCACCGGAGAGATTTGAGGACCACATTACATA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                              CTCATGTTGGTGGACGAGAGGCAGATGCACATCGAGCAACTGGGCCTGCAGAGAAA
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GAAAACGCTAAAGCGGCTCAACAAACTTCGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCC
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	3992 CTCACGAGTTGTGAAGCCCTCAATATCGTCACGGAGAGATTTGAGGACCACATAAAAA 1051
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1813 GAACTGAGCTGCAGTGTAGACTTACTAAAGAGCGGCTTGATGCCATAAAGAGGGGTAGAA 1892 1919 AGGGAGTGAGTTAAACCAAGTGTACTAAAAGAGGGTTGATGCCAAAACAATTTAAACAAGAAACAATTTAAAAGAGGTTGAAACAATTTAAAAAAAA	

qq	3234 CATCTGAGCCTGTTTCCTCATCAGTTAGATGTGGGGACTCAATCACA 3280
ò	4052 IGCTCCCAAAGGCTGGCTCCCAATTTTCCTAAGTGCAACTTTAATAGACTCAGTT 4111
qq	3281 CGCTCTTCAAGTCCGGCTCCCATATTTCCTAATTGCAAGCCAAATTTAATGTACCTTGTT 3340
ò	4112 CTGTGAT-TTTTTTTCCAAAAAAAAAAATATTTTGAAATAGGACAGAGGGTTAACAGTTGT 4170
Ор	3341 CCACAATAATTTTTTTTTTTAAAAAATCCTATTACAAAATAAGACATACTTTAAACTATTGT 3400
ò	4171 CATTITGCACTATCAAGCCATGAGTITTGATAATGAGTTATAAGAAA-AGAATACTITCA 4229
Ор	3401 CATTIGCTCTTTCACATCAGAATTIGCTTTATGTGCTGGAAAAACATCACATAGCTA 3460
ò	4230 GAGCTATCACAGGGTCTCTAAACTTTTGGAAAAACAAAAGCCCCTAATATGACCTCAGGA 4289
qq	3461 TCACAGGGCCTGGACCTCTAAAATTTTGCAAAAACAAAAGGTTCTAAGATGATTTCAGGA 3520
ò	4290 AACAATTTGAACATGAAATAGAAATGGAATGAACTGTG 4327
q	3521 AATAATGTGAACATGTAATAAAATGGAAATGAAATATG 3558



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September 7, 2004, 21:24:04; Search time 323 Seconds (without alignments) 7497.850 Million cell updates/sec
                                                                                                                                                                  GenCore version 5.1.6 . Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        682709 segs, 277475446 residues
                                                               - nucleic search, using sw model
                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                       Scoring table:
                                                                 OM nucleic
                                                                                                                                                                                                                                                                                        Searched:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\* Issued\_Patents\_NA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence	456 Sequence 10456,	Sequence	1 Sequence 1,	Sequence 1,	Sequence 1,	Sequence 20,	Sequence 20,	Sequence 20,	Sequence 2, 1	Sequence 2,	m	Sequence 2, Appli	7	Sequence 1,	4 Sequence 14,	Sequence 1,	Sequence 1,	Sequence 15,	Sequence 15,	Sequence 15,	5 Sequence 15,	Sequence 15,	5 Sequence 15,	Seguence 48,	
SUMMARIES	. QI	US-09-620-312D-1065	US-09-621-976-10	US-08-232-463-1	US-08-728-323A-	US-09-298-568-1	US-09-410-399-1	US-08-770-379-20	US-08-757-669A-20	US-09-230-371A-20	US-08-875-435B-2	US-09-249-585A-2	US-09-410-399-3	US-09-050-863-2	US-09-359-081-2	US-09-130-114-1	US-09-647-344A-1	US-08-910-647-1	US-09-620-925-1	US-07-884-811-15	US-07-885-971-15	US-08-087-783A-1	US-08-194-088B-1	US-08-194-087-15	PCT-US93-04648-1	US-09-724-566A-48	
de	Query Match Length DB	69.3 4892 4	3.0 418 4	2.3 7218 1	2.1 3489 2	2.1 3489 4	2.1 3489 4	2.1 32207 2	2.1 32207 3	2.1 32207 4	1.6 5919 4	1.5 1926 4	1.5 1926 4	1.5 2580 3	1.5 2580 4	1.5 5452 2	1.5 8705 4	1.5 9600 3	1.5 9600 4		1.5 10596 1		1.5 10596 1	1.5 10596 2	1.5 10596 5	1.5 16080 4	
	Score	3025.6	130	9.66	93.6	93.6	93.6	93.6	93.6	93.6	70.4	9:29	9.59	9.59	9.59	9.59	9.59	9.59	9.59	65.6	9.59	65.6	9.59	9.59	65.6	9.59	
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Sequence Seq	sednence
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6 6 6 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	70
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## ALIGNMENTS

	Gaps	AAGGAG
	4892;	GGTT-
	Length Indels	CCACTGGGTTCTTCAAGGGATAAACCAGCGGC-GAAAGAACACACCATTGGTT-AAGGAG
gg ang	DB 4; 734;	AAAGAAC
Mucleic Acids 620,312D	re 3025.6; d. No. 0; Mismatches	9-2992E
SULT 1  -09-620-312D-1065  Sequence 1065. Application US/09620312D  GENERAL INFORMATION:  APPLICANT: Tang, Y. Tom  APPLICANT: Liu, Chenghua  APPLICANT: Asundi, Vinod  APPLICANT: Ren, Rei, hong  APPLICANT: Ren, Rei, hong  APPLICANT: Rang, Yonghong  APPLICANT: Xue, Aidong J.  APPLICANT: Xue, Aidong J.  APPLICANT: Mang, Yonghong  APPLICANT: Mang, Yonghong  APPLICANT: Mang, Jian-Rui  APPLICANT: Mang, Dunrui  AUMBER OF SEQ ID NOS: 1105  AUMBR	8 8	TAAACCA
ULT 1  10-620-312D-1065  equence 1065, Application US/0962031  equence 1065, Application US/0962031  ERERAL INFORMATION:  APPLICANT: Liu, Chenghua  APPLICANT: Liu, Chenghua  APPLICANT: Liu, Chenghua  APPLICANT: Chang, Jie  APPLICANT: Chang, Jie  APPLICANT: Chang, Jie  APPLICANT: Chen, Rui-hong  APPLICANT: Chen, Rui-hong  APPLICANT: Wehrman, Tom  APPLICANT: Wehrman, Tom  APPLICANT: Wang, Jina-Rui  APPLICANT: Wang, Jina-Rui  APPLICANT: Mang, Jina-Rui  APPLICANT: Mang, Jina-Rui  APPLICANT: Mang, Jina-Rui  APPLICANT: Wang, Jina-Rui  APPLICANT: Wang, Jina-Rui  APPLICANT: Mang, Jina-Rui  APPLICANT: Wang, Shiwai  APPLICANT: Wang, Jina-Rui  APPLICANT: Wang, Jina-Rui  APPLICANT: Wang, Jina-Rui  APPLICANT: Wang, Jina-Rui  APPLICANT: Dohn Tillinghast  APPLICANT: Wang, Jina-Rui  APPLICANT: Dohn Tillinghast  APPLICANT: Dohn Tillinghast  APPLICANT: Wang, Jina-Rui  APPLICANT: Dohn Tillinghast  APPLICANT: Dohn Tillinghast  APPLICANT: Wang, Jina-Rui  APPLICANT: Dohn Tillinghast  APPLICANT: Dohn Tillinghast  APPLICANT: Dohn Tillinghast  APPLICANT: Wang, Jina-Rui  APPLICANT: Dohn Tillinghast  APPLICANT: Dohn Tillinghast  APPLICANT: Wang, Jina-Rui  APPLICAN	3#; 5#; 0	AAGGGA.
1065 MATION: MATION: MATION: MATION: MATION: Liu, Chenghua Asundi, Vinod Zhang, Jie Ren, Rui-hong Zhang, Jie Ren, Rui-hong Zhao, Qing A. Wahman, Tom. Xue, Aidong Zhao, Qing A. Wang, Jian-Rui Zhao, Qing A. Wang, Jian-Rui Zhou, Ping Mang, Zhuwei Mang, Zhuwei Mang, Zhuwei Mang, Zhuwei Mang, Zhuwei Mang, Zhuwei Mang, Zhuron Mang, Zhiwei John Tillinghast Mang, Zhiwei Mang, Zhiwei Mang, Zhiwei Mang, Zhiwei John Tillinghast Mang, Zhiwei Mang, Zhiwei John Tillinghast Mang, J	vat	GTTCTTC
SULT 1  1-09-620-312D-1065  Sequence 1065, Application US/ BAPELICANT: Tang, Y. Tom APPLICANT: Asundi, Vinod APPLICANT: Tang, J. Tom APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong APPLICANT: Chen, Rui-hong APPLICANT: Tang, Yonghong APPLICANT: Weng, Jian-Rui APPLICANT: Yang, Yonghong APPLICANT: Yang, Yonghong APPLICANT: Yang, Yonghong APPLICANT: Wang, Jian-Rui APPLICANT: Wang, Jian-Rui APPLICANT: Wang, Jian-Rui APPLICANT: Wang, Dinrui APPLICANT: Wang, DINRER: 09/ PRIOR FILING DATE: 2000-01-21 AVUMBER OF SEQ ID NOS: 1105 AVUMBER OF SEQ ID NOS: 1	Ë	CCACTGG
ULT 1  199-620-312D-1066  equence 1065. A  atent No. 65696  ENERAL INFORMATI APPLICANT: Tang APPLICANT: Asun APPLICANT: Cher APPLICANT: Wann APPLICANT: Wann APPLICANT: Wann APPLICANT: Wann APPLICANT: DA APPLICANT: Man APPLICANT: Man APPLICANT: Man APPLICANT: Man APPLICANT: Man APPLICANT: DA APPLICANT: DA  CURRENT FILING I  FILE REFERENCE: CURRENT FILING I  FRIGE REPLICATI PRIOR FILING DA  WUMBER OF SEQ I  ENGTH: 4892  TENGTH: 4892  TENGTH: ABMEXER: CDS  NAME/KEY: CDS  NAME/KEY: CDS  NAME/KEY: CDS  NAME/KEY: CDS  NAME/KEY: CDS  NAME/KEY: CDS	Query Match Best Local Si Matches 3593;	· ਜ
NESULT 1  US-09-620-312D-1065 Sequence 1065, Ap Sequence 1065, Ap Sequence 1065, Ap Sequence 1065, Ap APPLICANT: Targ, APPLICANT: Chen APPLICANT: Drag APPLICANT: Chen APPLICA	Query Best I Matché	λ̈
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3655 3715 4455 4037 3834 4397 3894 4277 3954 4678 4858 AGAGCTGAAGAAATCTGCAGCCAGCAGCACTGCCTCTTGGAGGGGGGAAGGGCTGAGG TAGAATTAATTAGCAGAATTTCTGTTTGCTGAATGTTCTGTTGAAGATGTTGGTCCAGTT AATCCTATTACAAAATAAGACATACTTTAACTATTGTCATTTGCCTCTTTCACATCATGA 3918 AAACGIGACAGCCGAAAAGGAGGIIIICACCACGGCACIGICCIICGCICTCCCCAGGAAICA CCTCTCCTAAGACCCGGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTCAC CCCAGGAGCAGGAAATCTGACCAAATTCGAGCCTCGAGCTGAGACTCAGTCTATGAAAT AGAGCTGAAGAAATCTGCAGCAGCAGCACCACCTCTCGGAGGGGGGAAGGGCTGAGG GCAGTGGCTAAGGGGGTATGTTGTGCAGATGCTACTGCTGCCGCGGAAAGTGAAACTTCAT AACCATTTAATAGCCATGCACCCCCTCCCATTTTGTGCATCTGTTTCAATGCAGGGGAA CA----AAATTAGCAAAACTATTGCTTGCTTGCTTAGAAGCCAGGGCGTGGTTTCTAGTTC rrrccrcarcagradargradacrcaar -- cacaccercraagrececercear TTTTGCAAAAACAAAAGGTTCTAAGATGATTTCAGGAAATAATGTGAACATGTAATAAAA cererececedecregardeaageaageageageacrareacearaacacegreae AACGTCATCCACACGAGGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGCCC TACCCCCACCCGCATTCCTATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGC CTCAGGAGCAGGAAATCTGACCAAATTCCAGCCTCGAGCTGAGACTCAGTCTATGAAAAT TITICCIAATIGIAAGCCAACTITAATAGACTCAGTICTGIGAT-TITITITCCAAAAA <u>artricctaatriccaagccaartriaargraccrrcriccacaaraartrirrraraaaa</u> AAAAATATTTTGAAATAGGACAGAGTTTTAACAGTTGTCATTTTGCACTATCAAGCCATGA GTTTGATATATGGGTTATAAGAAA-AGAATACTTTCAGAGCTATCACAGGGTCTCTAAAC ATTTGCTTTATGTGCTGGAAAAACATCACATAGCTATCACAGGGCCTGGACCTCTAAAA TTTTGGAAAAACAAAAGCCCCTAATATGACCTCAGGAAACAATTTGAACATGAAATAAAA 3978 4038 3476 3716 3356 3416 4098 4158 3656 4218 3776 3835 4398 3895 4456 4512 4194 3596 4278 4338 4015 4075 4134 4679 4253 4799 4313

RESULT 2 US-09-621-976-10456/c ; Sequence 10456, Application US/09621976 us-10-788-793-1.rni

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1655 GTTGAATAAAAACTTTAAGGTGGAGCAGGAAAAGTCATGGATGTGACGGAAAAGCTAAT 1714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1775 GACAAAGGAGGGGATGAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAGAAGGTCCTGTGA 1834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1895 GGAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAA 1954
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Patent No. 5948676

Patent No. 5948676

APPLICANT: Chang, Yuan

APPLICANT: Russo, James J.

APPLICANT: Russo, James J.

APPLICANT: Relaman, Isidore S.

APPLICANT: Russo, James J.

APPLICANT: Relaman, Isidore S.

APPLICANT: Relaman, Isidore S.

APPLICANT: Relaman, Isidore S.

TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Barcoma-Associated Herpesvirus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21

CORRESSONDEROES 21

CORRESSONDEROES 22

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 99.6; DB 1; Length 7
Best Local Similarity 1.6%; Pred. No. 1.9e-14;
Matches 6; Conservative 264; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
CUTMTRY: New York
CUMTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1955 GATCAGAGAACTAACGCT 1972
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1074 RRRRRRATCGCAAGCT 1057
                                                                                                         TELEX: 899149
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                  TELECOMMUNICATION INFORMATION:
                                                 TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                         ) IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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STREET: 1185.
CITY: New YORK
STATE: New YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 ACATGCTGAAGACAGAGAAAACCAAGCCTGAGGTTCTGGAGGCTCATTACGGGTCTGCGG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 AGCCAGAGAAAGTGCTGCGGGTCCTGCACCAGAGATGCCATTCTTGCCCAGGAGAAATCCA 152
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## Patent No. 6639063
## GENERAL INFORMATION:
## APPLICANT: Dumas Milne Edwards, J.B.
## APPLICANT: Dobert, S.
## APPLICANT: Jobert, S.
## APPLICANT: Jobert, S.
## APPLICANT: Glordano, J.Y.
## TITLE OF INVENTION: ESTS and Encoded Human Proteins.
## FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: U$/09/621,976
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
## SOFTWARE: Patent.pm
## SEQ ID NO 10456
## ILENGTH: 10456
## ILENGTH: JULY 10456
## ILENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
ADDRESSEE: Foley & Larcher
ADDRESSEE: Foley & Larcher
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PAPPLICATION UMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
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US-09-621-976-10456
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ZIP: 22313-0299
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; Patent No. 6322792
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Matches 415; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           Score 93.6; DB 2;
Pred. No. 4e-13;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/52268/C
TELECHONE: 212-278-0400
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 44.6%;
Matches 415; Conservative (
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US-08-728-323A-1
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1359 AAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGC 1418
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GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT PILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER PILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VET. 2.0
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44.6%; Pred. No. 4e-13;
tive 0; Mismatches 509;
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1897 GATGAGCÁGCÁGCÁGCÁGCÁGCÁGCÁGGÁTGÁGCÁGCAGCAGGÁTGÁGCÁGCÁGCÁG 1956
        699 AGGTTGAAAAAGCTCCTTGAACAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAAA 758
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STREET: 1185 Avenue of the Americas
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APPLICANT: Chang, Yuan APPLICANT: RUSSO, James J.; APPLICANT: RUSSO, James J.; APPLICANT: ROSO, James J.; APPLICANT: ROSO, James J.; TITLE OF INVENTION: PATICK S.; TITLE OF INVENTION: PATICK S.; VUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
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                                                                      999 ITITCCCAGGAGCACGAAGAATGAACGCCAAATTGGCGAATCAAGAATCTCACAACCGG 1058
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                                                                                                         2191 CAGCAGGATGAGCAGCAGCAGGATGAGCAGCAGCAGCAGGATGAGCAGCAGCAGCAG 2250
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939 AAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACACAAGGCCTCGAGG 998
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2.1%; Score 93.6; DB 4; Length 3489;
Best Local Similarity 44.6%; Pred. NO. 4e-13;
Matches 415; Conservative 0; Mismatches 509; Indels 6;
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
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CURRENT PILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
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APPLICANT: COCTEC, Murray A.
TITLE OF INVENTION: Methods to Inhibit C
TITLE OF INVENTION: to Genomic Host DNA
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Patent No. 6482587
GENERAL INFORMATION:
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SOFTWARE: Pat
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US-09-410-399-1
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759 GCTAAGCGGCTCAACAAACTTCGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCCCTCATG 818
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                  GAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAGGTCTGCGCCAAGCGCGTGCTTGAG 1238
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6183751
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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TITLE OF INVENTION: SE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
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: U.S.A.
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Pred. No. 1.3e-12;
0; Mismatches 509; Indels 6;
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                              APPLICATION NUMBER: US/08/770,379
FILING DATE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              28,678
ER: 52342
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAK: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: double
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                               579 CTGCTGGCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGGAACGAGAAGCACAAG 638
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Sequence 20, Application US/09230371A Patent No. 6348586 GENERAL INFORMATION:

US-09-230-371A-20/c

Chang, Yuan Bohenzky, Koy A Russo, James J Edelman, Isidore S Moore, Patrick S

APPLICANT:
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20220 GAĞCCACAGCAĞCAĞGATGAGCAĞCAGCAĞATGAĞCAĞCAĞCAĞGATGAĞCAĞCAĞCAĞ 20161
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TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: 45185-G-PCT-US CURRENT APPLICATION NUMBER: US/09/230,371A CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: PCT/US97/13346 PRIOR FILING DATE: 1997-07-22
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2.1%; Score 93.6; DB 4; Length 32
Best Local Similarity 44.6%; Pred. No. 1.3e-12;
Matches 415; Conservative 0; Mismatches 509; Indels
                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-20
                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.0
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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   1087 CGCAAAGGATTGAGGAGCTGGAAGAGACCAATAAAAGCCTTCAGAAGGCAGGGAAGAG 1146
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                                                                          TGCAGCTNCAAGAGGANCTNGCNGCNGCNGAGAGNGCTCGCAANCANGCNGACNTNGAGA
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Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: HOLICK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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LOCATION: (1)..(1926)
OTHER INFORMATION: coding strand of EBNA-1
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                                                                                                                                                    19446 GTGGAAGAGCAAGAGCAGGAGCAGGAAGAGCAGGAATTAGAGGAGGTGGAGGAGCAAGAG 19387
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                                                                              AAGAGGATGTCTGAGGTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGC
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Patent No. 6593304
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OTHER INFORMATION: n = A,T,C or G
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Similarity 37.2%;
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Best Local Similarity 37.2
Matches 413; Conservative
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                                   906 GAAGAAAAACTTCAAAGCGGTCACTTACAAATCCAAGGAAGACGCCAGAAGCTGCTCAAG 965
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APPLICANT: Hang, Betty
APPLICANT: Hang, Betty
APPLICANT: Hang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SUCHENCES: 5
CORRESPONDENCE ADDRESS:
0; Mismatches 339; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIN:
APPLICATION NUMBER: US/09/050,863
FILING DAIE: 30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Sequence 2, Application US/09050863
// Patent No. 6114111
// GENERAL INFORMATION:
Matches 269; Conservative
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                                                                                                   906 GAAGAAAACTCAAAGGGGTCACTTACAAATCCAAGGAAGACGCCAGAAGCTGCTCAAG 965
                                                                                                                                                                                                                                                                          APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: to Genomic Host DNA CURRENT APPLICATION WHOSER. US/09/410,399
CURRENT APPLICATION NUMBER: US/09/410,399
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                       1.5%; Score 65.6; DB 4; Length 1926;
44.2%; Pred. No. 2.7e-06;
tive 0; Mismatches 339; Indels 0
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Pred. No. 2.7e-06;
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Patent No. 6482587
GENERAL INFORMATION:
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US-09-410-399-3
                                                                  Conservative
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US-09-249-585A-2
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Matches 269;
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US-09-410-399-3
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                                                                                                                                                                                          Score 65.6; DB 3;
Pred. No. 3.1e-06;
                                      A-65638/DJB/RMS
ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 791-1989
TELEPHONE: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       1.5%;
                                                                                                      LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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US-09-050-863-2
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US-09-359-081-2
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Sequence 2, Application US/09359081
Patent No. 6316223
GENERAL INFORMATION:
APPLICANT: Lao, Ying
Hiang, Betty

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1146 CTCCAGGAGCTGAGAGAGAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCG 1205
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TITLE OF INVENTION: Mammalian Protein Interaction Cloning
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                                                                                                                                                                                        COUNTRY: USA
ZIP: 9411.4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritt
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
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Pred. No. 3.1e-06;
0; Mismatches 339;
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-359-081-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/050,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relephone: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                         System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: unknown
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LENGTH: 2580 base pa
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Best Local Similarity 44.2%;
Matches 269; Conservative
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; Patent No. 59/6807
; Patent No. 59/6807
; APPLICANT: HOTLICK, Robert A.
; APPLICANT: Horalick, Robert A.
; APPLICANT: Dassam B.
; APPLICANT: Dobbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; FILE REFERENCE: 0867/10903031
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5452;
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Best Local Similarity
Matches 269; Conserv
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; ORGANISM: VEBNA
US-09-130-114-1
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US-09-130-114-1/c
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plectin - rat
  smooth muscle myos
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C;Species: Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Date: 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T18296
R;Guillen, N.
submitted to the EMBL Data Library, February 1997
A;Reference number: Z18865
A;Reference number: T18296
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Rocusion: T18296
A;Residues: 1-2139 <GUI>A;Residues: 1-2139 <GUI>A;Residues: EMBL:L03534; NID:g1850912; FID:g1850913; PIDN:AAB48065.1
                      nonmuscle myosin
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F;91-780/Domain: myosin motor domain homology <MMO>
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C; Superfamily
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cgg12 1/USFTO spool p/USIOTB8791/runat 07092004 134022 10821/app query.fasta_1.4551
-Q=/Cgg12 1/USFTO spool p/USIOTB8791/runat 07092004 134022 10821/app query.fasta_1.4551
-DG=FR 78 -QFMT=fastan -SUFFIX=rpr -MINMÄTCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=E1ts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-UOTFWH=pstp- -NORMSext -HEAPSIZEE=500 -MINIEN=0 -MAXENS=200000000
-USER=USIO798793 @CGN 1 1 218 @runat _07092004 134022 10821 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                            protein search, using frame_plus_n2p model
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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528 SerSerSerGluValileSerGlnHisLeuValSerTyrArgAsnIleGluGluLeuGln 547
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568 GluGlnGluThrThrSerSerLys1leThrGluLeuGlnLeuLysLeuGluSerAlaLeu 587
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A;Residues: 1-31,'R',33-142 <KIN>
A;Cross-references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256
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A;Map position: 1q25-1q25
A;Introns: 177/3
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A;Accession: G01185
A;Status: translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 144-228 <GRE>
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Nalternate names seriolated transforming protein (tpr-met); protein with promoter (S. Alternate names)
C. Species: Home sapiens (man)
C. Species: Home sapiens (man)
C. Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 11-Jan-2002
C. Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 11-Jan-2002
R. Mitchell, P.J.; Cooper, C.S.
Oncogene 7, 2329-2333, 1992
Oncogene 7, 2329-2333, 1992
A. Fitchell, P.J.; The human tpr gene encodes a protein of 2094 amino acids that has extensive cointy A. Reference number: $33124; MUID:93064711; PMID:1437155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-2094 <MIT>
A;Cross-references: EMBL:X66397; NID:g633225
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
                                                                                                                                                                                                                                                                                                                                                   ||| ::::::
1642 IleLysArgLysGlyLeuGluGluGluValLysLysLeuThrThrGluIleGlnAlaLeu 1661
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                                                                                                                         ------GAAGAC 2288
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1662 LysPheGlnIleAsnAlaProSerSerValAlaGlnGluGluGlu-LysGlnArgLeuGl 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2462 CGTGCCTGTGGCCTCCACTGGGGTGCAAACCGAGGCGGTGTGCGGGGATGCTGCGGAAGGA 2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1681 uSerAspIleAlaGluLeuLysGluGinLeuGluGlnGluArgThrThrAlaAlaAsnAl 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CTGAAGAACCCATGGAACGGTC 2620
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1717 eAsnLeuGluAspValThrAsnGlnArgGluLysLeuValAlaLysAsnSerGluAsnAs 1737
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|1602 AspAsnAspLeuThrSerLysIleGluIleThrGluAsnGluMetLysLysLeuGluAsn
                                                                                                                                                                                                                                                                                                               2349 ACTAAGAACAAGAACATGGGGAGGGTCCTCAATCTGACCAAGGAGCTAGAGCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2522 GGAGACCCCGGCTGTTCATTCGCAAATCCTTCCAGGAGA---AATCACATGAG
                         CGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAGAAG
                                                                    GluMetLysGlyValGlnAsnAsnGlnLeuGinAlaThrAsnLysGluLeuLysAlaLys
                                                                                                                                                                                                                       CAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                  ---TTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID:g37258 R;King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J. Oncogene 2, 617-619, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Titi: Noticetide sequence analysis of human tpr cDNA clones. A;Reference number: $23740; MUID:92195670; PMID:1549355 A;Accession: $22740
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A;Reference number: S00928; MUID:88262257; PMID:3387099
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A;Residues: 1-725,'L' <MI2>
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Oncogene 7, 383-388, 1992
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пр		ДD	1118 GlnLysAlaG
ò		λ	1548 AGCCTCAAAG
q	SerGluValArgLeuSerGlnGlnArgGluSerLeu	qq	1137 MetLeuLysA
ò		δλ	1587 GTGATGCTGG
ОР		qq	1157 ArgheuleuH
ò		ò	1647GTGGATG
qq		QQ	1177 GlyvalGlnd
ò		ò	1692 ATGGATGTG-
Db		qq	1197 LeuGluileLe
ò	936 TCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACAAG 989	λo	1728
Db		q	1217 AlaGlnValG
ò	990 GCCTCGAGGTTTTCCCAGGAGCACGAAGAGATGAACGCCAAA1031	ò	1758 GAAAAGGAGTA
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ò		ò	1788GA
Db		qq	1257 AlaGlnHisGl
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οp		qq	1354 TyrArgLysLe
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1485	S GTGGTCAAGAGTCGAGTTAAAGAA 150 	508
1508	TCCGAGAGTAGACTGGAGAAGGCCGAGTTA 15	547
1548	11	586
1587	AATAAAGCAAGAAGAGAAA 16  -:-: svalvalAlaServalLysGlu 11	546
1647	GTGGATGGGTTGAATAAAACTTTAAGGTGGAGCAGGGAAAAGTC 16	591
1692	17	727
1728	8	157
1758	GAAAAGGAGTACCAGTCTCACAAAGGAGG	87
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31	ACTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGGGGGGGGG	א וס וי
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2009	200	60
1374	GlulleGlyArgLeuLysAlaGluIleAlaArgSerAsnAlaSerLeuThrAsnAsnGln 13	93
2010	CAGGTGGTGGAGGGGGACTTGATGAAGACCGAGGACGAATATGAC 205 ::: :::::	54
2055	GAAGTICAGAACCGAGGAGATAAGGCAAACTICCTCTCCCAG 210	33
2109		38
2139	CACAAAGCCATAGAGAAAGGGAAAGCGAA	S

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 	2166 GCCGTGAGCCGAAGCCGAACTGCGACAGGTTTCGGCTGGAGGCTAAAAGTCGT 2225	2226 GATTTACAGGCCGAGGTGCAGGCTCTCAAGGAGAAGATCCACGAGCTG 2273	2274 ATGAACAAGGAAGACCAGCTGTCTCAAGTCGACTATTGGGTCCTTCAGCAAAGA 2333	TTTATGGAAGAAGAAACTAAGAACAAGAACATGGGGAGGGA	1532 LeuGinAspArgThrThrGinGluGluGlnLeuArgGinGinileThrGiu 1548 2394 GAGCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGG 2453	:::	2454 ATGGTGGACGTGCCTCCACTGGGGTGCAGACCGAGGGGTGTGCGGGGATGCT 2513	GCGGAGGAGAGACCCCGGCTGTGTTCATTCGCAAATCCTTCCAGGAGGAAAATCACATC 257	1574 LeuThrLysGluAsnGluGluLeuLysGlnArgAsnGlyAlaLeuAspGlnGlnLysAsp 1593	2574 ATGAGTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTC 2630 :::::	2631 GACAGGTATCCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATG 2690	1614 GluArgGluLeuArgGluHisGlnGluArgHisLeu 1625	2691 AGAAAAGGGGCCTTCCACTCCGCAGGAGAAGGGCCCAGGCCAAACCAGGGT 2750 18:1	2751 GCAGGGCACCCCGGGGAGCTGGTCCTAGCACCAAAGCAGGCCAGCCCCTACACATCCGT 2810		2811 GTGACACCAGATCATGAGAACAGCACTGCCAC 2843	IIII IIII FIOALASEICLYGINAIGGIYIIEALASEIIIISEIABPFIOFIOINKALAABN CTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTCTCTAGTACCACCGTCATTCCTACC	::::::     	2904 TTAGGCAACCAGAAACCAAGAATAACCATTATTCCATCACCCAATGTCGCAA 2960	1687 AlaGlyAsnLysSerThrProArgAlaSerlleArgPro	AAGCCCAAAAGTGCAGATCCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATT	ProAlaThrValThrAsnProThrThrThrProThrAlaThrValMetProThrThrGln	ACTACTATTICCAGAGAGAGACCCGGAAGGIGGAAGGAGCGCCTTIGCCGACAGGCCT	ValGluSerGinGluAlaMetGlnSerGluGly	3081 GCATCCCCCATCCAACTCATGAGGGGTGTCAAATCTGCAGCTCCCCATGAATGGCTGCT 3140	3141 TCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCGGAAAA 3200
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omere protein E - human entromere 312K protein; kinesin-related protein CENP-E cies: Homo sapiens (man) entromere 103-mar-1994 #text_change 19-Jan-2001 ession: 52861; A. T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W. e 359, 536-539, 1992 elec CENP-E is a putative kinetochore motor that accumulates just before mitosis. ession: S28261; MUID:93024922; PMID:1406971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3321 GAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAGGAGGTT 3380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3381 TCTACAGGCACAGTCCTTCGCTCTCCCAGGAACCACCTCTTCAAGACCCGGTGCTAGC 3440
                                                                                                                                                                                               -------AlaThrAlaPheValGlnProThrGln 1780
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1835 GluGluAspSerThrIleGluAlaSerAspGlnValSerAspAspThrValGluMetPro 1854
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1855 LeuProLysLysLeuLysSerValThrProValGlyThrGluGluGluValMetAlaGlu 1874
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1752 SerProAsnValGlnPro---SerIleSerGlnProIleLeuThrValGlnGlnGlnThr 1770
                                                                                                    3201 CAAACTGTTCCAGCCCCCGGGGAAGTACAACTCCAATGCTAATATCATCACCACGGAA 3260
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88-references: EMBL:Z15005; NID:g29864; PIDN:CAA78727.1; PID:g29865 etics:
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20.61%
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                                                                                                                                                                                                    1771 Gln----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3459 -----
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993 TCGAGGTTTTCCCAGGAGGAGGAGGAGGACCCAAATTGGCGAATCAAGAATCTCAC 1052 :::	1158 AGAGAGAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGGGGAAGTGGAGAGT 1217 :::   :::::: 1773 GINGluGluLeuArg1leAlaHisMetHisLeuLysGluGlnGlnGlnThrIleAspLys 1792 1218 CTGCGCAAGGCGTGCTTGAGATGGAGGCCAAGGATGAAGATCACG 1265	AsnSerAsnAlaLysLeudlnGluLysIleGlnGluLeuLysAlaAsnGluHisGlnLeu AAGGAACTTAGACTAGAAGTGAAGAGAGAAGCTGAAGAGCTGAAGCTGAAGCTGAAGAAGCTG	1431 CTGAACCTGGAGAAGGAGAACCTAACCAACCTGCTGAACGAGCTGGAGGTGGTC	1602 GAGAGGAAAATTGATGGAGAAAATAAAGGAAGAAGAGGAAAGTGGATTGAAT 1661	1782 GAGAGGATGAGCTGAACTGAGGAGCGAAGAAGAAAGACTGAACTGAGC 1841
8 6 6 6 6	8 8 8 8	8 6 6 6	8 6 6 6 6	8 6 6 6 6	8 8 8 8 8 8 8
Query Match:         6.12*         Indels:         389           DB:         1         Gaps:         64           US-10-788-793-1         (1-4364)         x S28261         (1-2663)           QY         171         TCAGAAGATGCAAAAAGAACAAGGCCAATCGGAAGGAGGAGGAT		Db 1462 LysGludsnileLysGlulleValAlaLysHisLedGluThTGluGluGluGluceLysVal 1481  Qy 408 GCACACTATGGATCTGCAGAAGTGCTTGGGTCTTGGACCGAGATGCCATC 467	Oy         525 GACAGACTGGAGGAAAAGCAGAAGGAAGGTACCGCGGCTGTGTGTG	651 ATGAACAAGAGGACGACTTCACCAACCTGCTGGAGCAGGGGGAGAGGGTTGAAAAG  651 ATGAACAAGAGGACGACTTCACCAACCTGCTGGAGCAGGGGGGGG	90 810 GCCCTCATGTTGGAGGAGGCAGATGCACTGACTGACTGAC

N;Contains: myosin ATPase (EC 3.6.4.1) C;Species: Gallus gallus (chicken) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002	Oy 446 GGTCCTGCAC                 953 ulleLeuHis	GGTCCTGCACCGACATGCCATCCTTGCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGA 505 
Cyncolesion: 943-942; A43-940. K;Takahashi, M.; Kawamoto, S.; Adelstein, R.S. J. Biol. Chem. 267, 17864-17871, 1992 A;Title: Evidence for inserted sequences in the head region of nonmuscle myosin specific	Qy 506 GAAACCT  ::: Db 965 uGluGlu	GAAACCTATCTCAGAGCTGGACAGACTGGGGAAAAGCAGAAGGAGAGGAGGGTGCGGCCGCAT 565  :::
	Oy 566 GCTAGAG               	
A)restructs: 1.2007 (1918) A)2076; NID:g212448; PIDN:AAA48988.1; PID:g212452 A;Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide set A;Accession: A43402	Qy 626 CGAGAAG               Db 1002 uGluLys	ACTI 1:1
2449	Qy 686 GCAGGAG   ::: Db 1022 uAspGln	GCAGGAGCGAGGAGGTTGAAAAAGCTCCTTGAACAAGAAAÀ 727   ::
ydrd MYN);	Qy 728 AGCTTAC Db 1042 sThrSer	AGCTTACCAAGCCCGCAAAGAAAAGGAAAACGCTAAGGGCCCAACAAACTTCGAGATGA 787
Le	Qy 788 GCTTGTGJ Db 1062 8	GCTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGACGAGGGGAGATGCACATCGA 847 : 8
<pre>f,332-552/Region: actin binding #scarus predicted F;632-652/Region: alternatively spliced segment 2 #status experimental F;652-714/Region: actin binding #status predicted F;875-2507/Domain: colled coil #status predicted <coi></coi></pre>	Qy 848 GCAACTGC Db 1063	GCAACTGGGGCTGCAGAAGTCCAGGACCTCACTCAGAAGCTGAGGAGGAGGAGA 907 
F.1316-2007/Region: 1ight meromyosin F.1316-2007/Region: 1ight meromyosin F.129/Modified site: NG.NG.NG-trimethyllysine (Lys) #status predicted F.184/Binding site: ATP (Lys) #status predicted F.732,742/Active site: Cys #status predicted	Oy 908 A     Db 1078 uLysThr#	A
P;1954/Binding site: phosphate (Thr) (covalent) #status predicted F;1987/Binding site: phosphate (Ser) (covalent) #status predicted alignment scares.	Qy 950 CCAG1     : Db 1098 uGlnAspC	CCAGAAGCTGCTCAAGTTACAAGTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCA 1006
Pred. No.: 1.43e-14 Length: 2007 Score: 471.50 Matches: 270 Percent Similarity: 40.82  Conservative: 257 Best Local Similarity: 20.91 Mismatches: 488	Qy 1007 GGAGCACC :::: Db 1118 sLysGlud	GGAGCACGAAGAGATGAAGCGCCAAATTGGCGAATCAAGAATCTCACAACCGGCA 1060 ::::
f.10% Indels:	Oy 1061 ACTTCGAC	ACTICGACTCAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCT 1105
US-10-788-793-1 (1-4364) x B43402 (1-2007)  QY 101 AAGTTCATCTAACGGGGATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGGTGATGGTGG 160	1106	
Db 848 LysIleLeuGlnArgAsnCysAlaAlaTyrLeuLysLeuArgHisTrpGlnTrpTrp 866 Oy 161 TAAGGGCCCTCAGAAGATGCAAAAAGAAGACCAATCGGAAGGAGGAGGATGTCAT 220 Db 627 Andrian Dreman Comment Comme	1166	AATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGAGGGGGGTCTGCGAA 1225
221 GGCTTCCGGAACTATCAAAAGGCACCTCAAACCATCTGGAGAAAGTGAGA [	Qy 1226 GCGCGTGC   Db 1189Thri	GCGCGTGCTTGAGATGGAGGGGAAGGATCACGAAGACCGAGGCCCAGTG 1282    :::
281 GAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAG	Qy 1283 CCGGGAGC         Db 1207 lAlaGluI	CCGGGGGGCTGAAGAAGTCCCAAGAGGAAGAACACCACAGCAAGGAACTTAGACT 1339
GACAGAGAA	Qy 1340 AGAAGTGG       Db 1227G	AGAAGTGGAGGAGGAGAGGATGTCTGAGCTGGAGAAGCTGGAGAAGCTTCAG 1399 
386 AACCAAGCCCGAGGTTCTGGAGGCACACTATGGATCTGGAAACTGAGAAAGTGCTTCG :::	1400	TCGGAATGCACCCAGCTCCATCTGAACCTGGAGAAGGAGAAG :::
	Oy 1452AACC	AACCTAACCAAAGACCTGCTGAACGAGCTGGAGGTGGTCAAG 1493

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128 152 130 158	SCAAGAAGAGAA 1645 :::	ATAAACCGAGGTAGGTC 1915    :::AsnLysLysLysLe 1428 AGAGAACTAACGCTTGA 1975	### CAGAACCGAGCAAA 2095  ###################################	CGGCTGGA 2209         ValHisGluLeuGl 1562         ::::::        :::        :::
	<pre>5 TGTGATGCTGGATGGAAAATATGATGGAGAAAATAAAGCAAGAAAGGAAGG</pre>			
	Oy 1586 Oy 1318 Oy 1646 Oy 1333 Oy 1706	Oy 1875 Db 1413 Oy 1916 Db 1428 Oy 1976 Ob 1445	Qy     2036       Db     1465       Qy     2096       Db     1484       Qy     2145       Db     1502       Qy     2168       Db     1522       Db     1522	Oy 2202 Db 1542 Oy 2210 Db 1562 Oy 2270 Db 1581 Oy 2318

||| ||| :::::: 1660 uGluGlyGlnIleGluAlaAlaAsnLysAlaArgAspGluAlaIleLysGlnLeuArgLy 1680 aSerGluArgAlaArgArgHisAlaGluGluArgAspGluLeuAlaAspGluIleAl 1749 1749 aAsmSerAlaSerGlyLysSerAlaLeuLeuAspGluLysArgArgLeuGluAlaArgIl 1769 1927 aAsnAlaSerArgArg-----LysLeuGlnArgGluLeuAspAspAlaThr---- 1942 1640 gLysGlnArgAlaLeuAlaValAlaAlaLysLysLysMetGluMetAspLeuLysAspLe 1660 2474 CTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCGGC 2533 2624 GGTCCTCGACAGGTATCCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCC 2683 2684 TTGGATGAGAAAAGAGAAAACGGTCCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCAAA 2743 2744 CCAGGGTGCAGGCACCCCGGGGAGCTGGTCCTAGCACCAAAGCAGGGCCAGCCCCTACA 2803 2864 ATCTGAAGAGTTTTTCTCTAGTACCACCGTCATTCCTACCTTAGGCAACCAGAAACCAAG 2923 1804 ------LeuAlaGlyGluArgSerAlaAlaGinLyBSerGluAsnAlaArgGlnGl 1820 3044 CCCGGAAGGTGGA---AGGAGCGCCTTTGCCGACAGGCCTGCATCCCCCATCCAAATCAT 3100 |||||| |1834 uLeuGludlySerValLysSerLysPhe---------LysAlaThr1leSe 1848 3161 GCCTATGGGAAGGACTATCCTCAAAGTCACCCGGAAAAA---CAAACTGTTCCAGCCCC 3217 n'alGluAspGluArgArgHisAlaAspGlnTyrLysGluGlnMetGluLysAlaAsnAl 1908 1908 aArgMet---LysGlnLeuLysArgGlnLeuGluGluGluGluGluGluAlaThrArgAl 1927 CTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGACGTGCCTGTGGC 2473 2567 TCACATCATGAGTAATCTTCGACAGGTAGGCCTGAAG---AAACCCATGGAACGGTCCTC 2623 2804 CATCCGTGTGACACCAGATCATGAGAACAGCACTGCCACCCTGGAGATCACAAGCCCCAC 2863 2924 AATAACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCAAAAGTGCAGATCCTAC 2983 2984 TCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGAGAGAAGAG 3043 3101 GACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAGGAAGT 3160 3218 CGTGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGACAATAAAATTCACAT 3277 3278 TCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCAGT 3337 3338 TATCACCGTCCGGCCTGTCAACGTGACAGCGAGAAGGAGGTTTCTACAGGCACAGAGTCCT 3397 1601 nAlaMetLysAlaGlnPheGluArgAspLeuGlnAlaArgAspGluGlnAsnGluGluLy 1621 GAACAAGAACATGGGGAGGAGGTCCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCG

us-10-788-793-1.rpr

F;125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted   F;185/Modified site: ATP (Lys) #status predicted   F;186/Binding site: ATP (Lys) #status predicted   Alignment Scores: Cys #status predicted   Alignment Scores: 1.76e-14   Length: 228   Scores: 469.50   Matches: 228   Percent Similarity: 41.02   Conservative: 181   Cuery Match: 181   Cuery Match: 181   Cuery Match: 181   Cuery Match: 191   Cuery Match: 191   Cuery Match: 1   Cuery Match: 191   Cuery Match: 1   Cuery Match: 1	"ACATGCTGAGGACAGAGAAACCAAG
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Oy 2643 CCAGCAGGAATGAGG Db 1690 LeuAlaAlaAlaGlul Oy 2703 AACGGTCCTTCCACTC Db 1701 Oy 2763 GGGAGCTGGTCCTAC Oy 2763 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		8 4 8 6 8 6 8 6
2505 1670 2643 1690	GAAAAGGAGTACAGTCTGACAAAGGAGAGGATGAGCTGATGGGTAAACTGAGGAGCGAA :::	6 6 6
1630 2565 1650	1638 GAGAGGAAAGTGGATGGGTTGAATAAAACTTTAAGGTGGAGCAGGGAAAAGTCATGGAT 1697  :::            :::    1293 AspSerLysSerSerLysLeuThrLysAspPheSerAlaLeuGluSerGlnLeuGlnAsp 1312  1698 GTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAG 1757             :::::::::     1313 ThrGlnGlubeuLeuGlnGluGluAsnArgGlnLysLeuSerLeuSerThrLysLeuLys 1332	8 6 8 6
Db 1597 AlaGluLeuGlu Oy 2451 AGGATGGTGGACGTG Db 1616 LeuGluMetAspLeuI Oy 2511 GCTGCGGAGGAGGAG		8686
OY 2331 AGAITTATGGAAGAA(		è e
	1452 AACCTAACCAAAGACCTGCTGAACGAGCTGGAGGTG 1487 	\$ 6
	1332 CTTAGACTAGAAGTGGAGAAGTGCAGAAGTGTCTGAGCTGGAGAAGTGGAGGAA 1391	8 8 8 8
1497 GluArgLeuAsnL		o d
Qy 2130 CAAATGGCCAAGCAC) Db 1481 Serbeuala	AAGACCGAGGCCCAGTGCCGGGAGCTGAAG L          LysThrGluLeuGluAspThrLeuAspSerThrAlaAlaGlnGlnGluLeuArgSerLys	ò qa
	125 AlaSerArghanLysalaGluLysalaGluLysalaGluGluGalu	8 6 8
Oy 2004 CAGTTGGAG Db 1421 GlnGluLeuAspAspl Ov 2031 ATGAAGACCGAGGAC		à d

:|||:::||| gAspArgAlaGluAlaGluAlaArgGluLysGluThrLysAlaLeu 1480 CAAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCCGAACTG 2189 :::|||::: |||| pLeuLeuValAspLeuAspHisGlnArgGlnSerAlaCysAsnLeu 1440 -----GAGCAGAAG 2069 GGATAAGGCAAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAACAC 2129 :::|||:::||| -ArgAlaLeuGlu-----GluAlaMetGluGlnLy8AlaGluLeu 1496 :::|||||| sGlnpheArgThrGluMetGluAspLeuMetSerSerLysAspAsp 1516 :::: |||||| :::::: nLeuGluGluLeuGluAspGluLeuGlnAlaThrGluAspAlaLys 1556 CGACTATTCGGTC-----CTTCAGCAA 2330 lAsnLeuGlnAlaMetLysAlaGlnPheGluArgAspLeuGlnGly 1576 AGAAACTAAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTGACC 2390 ||| ||| ||| ||| si: |||:::||| si: rgluglufysLysLysGnLeuValArgGnValArgGluMetGlu 1596 TTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGA 2450 :::||| -AspGluArgLysGlnArgSerMetAlaValAlaAlaArgLysLys 1615 3CCTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGAT 2510 . JLys-------AspLeuGluAlaHisIleAspSer 1629 GACCCCGGCTGTGTTCATTCGCAAATCCTTCCAGGAGGAA---- 2564 ||| ::: gAspGluAlaIleLysGlnLeuArgLysLeuGlnAlaGlnMetLys 1649 siysleulysSerMetGluAlaGluMetileGlnLeuGlnGluGlu 1689 TCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACCCC 2762 |||||||:: |-GlnGlnGluArgAspGluLeuAlaAspGluIleAlaAsnSerSer 1715 ------GAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAG 2246 BAAG---AAACCCATGGAACGCTCCTCGGTCCTCGACAGGTATCCC 2642 GATCCACGAGCTGATGAACAAG------GAAGACCAGCTG 2294 C;Date: 22-Nov-1993 #sequence\_revision 02-Dec-1994 #text\_change 09-Jun-2000 AGCACCAAAGCAGGCCAGCCCCTACACATCCGTGTG 2813 malaria parasite (Plasmodium falciparum) -AGGTTTCGGCTGGAG-----CGAATATGACCAGTTG------

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1019
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1145 GlnGluGlnSerAspLeuGluGlnGluArgLeuAlaLysGluLysLeuGlnGluGln 1164
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1245 LysLeuGlnGlnGlnSerAspLeuGluGlnGluArgArgAlaLysGluLysLeuGln 1264
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                                                                           CAGCTGCTGCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAG
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986 LeuAlaLysGluLysLeuGlnGluGlnGlnSerAsp------LeuGluGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CTTGAACAAGAAAAGCTTAC
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|1073 LysGluLysLeuGlnGlyGlnGlnSerAspLeuGluGlnGluArgLeuAlaLysGluLys
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| |-------bysLeuGlnGlyGlnGlnSerAspLeuGluGluGluAlaLys
                                                                                                                                                           ------GACAGACTGGAGGAAAAGCAGAAGGAGGACGTACCGCCGCATGCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                               633 CACAAGCACACTGACTACATGAACAAGAGGGACGACTTCACCAACCTGCTGGAGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1002 ArgLeuAlaLysGluLysLeuGlnGlyGlnGlnGlnSerAspLeuGluGluGluArg-----
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          CiACCEBBIOLE: S21897; ASS197; ASS193; S34842; B45592; C45592; D45592
R;ZUL, J.; Hollingdale, M. S.
B; Wolference number: S24597
A; Accession: A45592
A; Accession: A4592
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LysLeuGlnGluGlnGlnSerAspLeuGluGlnAspArgLeuAlaLysGluLysLeuGln 873
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|GluGlnGluArgLeuAlaLysGluLysLeuGlnGluGlnGlnArgAsp-----LeuGlu 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 GAAGATGCAAAAAAAAGACCAATCGGAAGGAGGAGGATGTCATGGCTTCCGGAACT
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Accession: S24597; A45592; S29393; S34842; B45592; C45592; D45592
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1422 CAGCTCCATCTGAACCTGGAGAAGGAAGAACCTAACCAAAGACCTGCTG 1472 :::	1473 AACGAGGTCGAGGTCGAGATCGAGATCACGAATGCTCCGAGAGTAGACTG 1532		:::     :::    :::	CTGGTGGATGAGGAAAAATATGATGGAGAAAATAAAGCAAGAAGAGGAAAGTGGAT	1320AspLeuGluGlüdlührgbeuAlalysGlülysLeuGlüGlüGlüGlüSerAsp 1337 1643 GGGTTGBATABABACTTTTBAGGTGGGGGABABATTTATGGATGGARGTGARAAGGTA 1719		1713 ATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGAAAAG 1763	1349 GlnGluGlnGlnSerAspLeuGluGlnGluArgLeuAlaLysGluLysLeuGlnGluGln 1368	1764 GAGTACAGTCTGACAAAGGAGGGGATGAGCTGATGGGTAAACTGAGGAGGAAGAAGA 1823 	AGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTAAAAGAAGCGGCTTGATGGC		1878 ATAGAGGAGGTAGAAAGGGGAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACC 1937			GTGGTGG				2097 TTCCTCTCCAGCAGCTCGAGGAAATCAAACACCAAATGGCCAAGCACAAAGCCATAGAG 2156 11	AAAGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGCCT		2217 AAAAGTCGTGATTTACAGGCCGAGGTGCAGGTCTCAAGGAGAAAGATCCACGAGCTGATG 2276	1505 GlnSerAspLeuGluGlnGlnArgArgAlaLysGluLysLeuGlnGlu 1520	2277 AACAAGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAA 2330			2390CAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGG 2441		2442 AACGGCCGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGGGTGCAGCGGACCGAGGCGGTG 2501
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.es: 71-846,'E',848-923,'K',925-1252,'I',1254-1318,'V',1320-1460,'S',1462-1580,'S
references: EMBL:L03188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use: 17:389, TTA', 392-724,'S',726-1790 <NDK>
references: GB:K54378; NID:94777; PIDN:CAA38253.1; PID:94778
references: GB:K54378; NID:94777; PIDN:CAA38253.1; PID:94778
references: GB:K54378; NID:94777; PiDN:CAA38253.1; PID:94778
references: Garden the Coden ACT for residue 768 as Ile
reference, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.
ed to the EMBL Data Library, February 1993
piption: An integrin analogue in Saccharomyces cerevisiae.
sion: S30782
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                                                                                                                                                        2502 TGCGGGGATGCTGCGGAGGAGGAGCCCCGGCTGTG------TTCATTCGCAAA 2549
                                                                                                                                                                                                                     2550 TCCTTCCAGGAGGAAAATCACATCATGAGTAATCTTCGACAGGTAGGCCTGAAGAAACCC 2609
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1638 LeuGluArgLysLysGluHisGlyAspValLeuAlaGluAspLeuTyrGlyArgLeuGlu 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ort protein USO1 - yeast (Saccharomyces cerevisiae)
nate names: protein D2552; protein YDL058w
es: Saccharomyces cerevisiae
12-Jul.1996 #sequence revision 12-Jul.1996 #text_change 21-Jul-2000
sion: S67593; A38455; $30782
ker, H.; Brandt, P.
ed to the Protein Sequence Database, July 1996
ence number: S67587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2610 ATGGAACGG-----TCCTCGGTCCTC----GACAGGTATCCC----
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ds: coiled coil; transmembrane protein
(2)Domain: transmembrane #status predicted <TMl>
()Domain: transmembrane #status predicted <TM2>
(3)Domain: transmembrane #status predicted <TM3>
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Qy 1151	Oy 1152 Db 1226	Qy 1197 Db 1246		1314 GAACACCACAGCAA 1::      1286 AspLysAsnSerLy	Qy 1329 Db 1306	Qy 1356CA 1326 LygGl	Qy 1386GAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCCAGCTCCATCTGAACCTG	Qy 1440 GAGAAGGAGAAGAACCTAACCAAAGAC          ::       Db 1366 GluLysGluArgLysLeuLeuAsnGluGlyS	Qy 1467 Db 1386	Qy 1494 AGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGTTAAGCCTC :::        :::::	Qy 1554 AAAGATGACCTTACAAAGCTGAAGTCCTTCACTGGATGCTGGTGGAGGAAA	Qy 1611 AATATGATGGAGAAAATAAAGCAAGAAGAGAAGGAAGGATGGAT	Qy 1671 AAGGTGGAGCAGGAAAAGTCATGGATGAGGAAAAGCTA	Oy 1713 ATCGAGGAAAGCAAGTTTTAAAACTCAAATCTGAAATGGGAAAAGGAGTACAGT :::	Qy	Qy 1830 Db 1519	Qy 1890	Db 1538Sex
	OS-IU-788-793-1 (1.4354) X S8/593 (1-1/90)  QY	219 ATGGCTTCCGGAACTATCAAAAGGCACCTCAAACCATCTGGAGAAAGTGAGAAAAAGACT 278	279 AAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGG 338	339 GAGTIGCAGGCTCGAGAAGATGTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAG 398	GTTCTGGAGGCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAAAAAAAA	GATGCCATCCTTGCTCAAAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCA	GAGCTGGACAGACTGGAGAAAAGCAGAAGGAGACGTACCGCGCGTGCTA ::::::::::::::::::::::::::::::::::::		630 AAGCACAAGACTGACTACATGAACAAGAGCGACGACTTCACCAACCTGCTGGAGCAG 689		Offile Self Leaded by Strucky	TTCGCCCTCATGTTGGTGGACGAGAGGCAGATCGAGCAACAGCTCGCAGAGT  TACGCCCTCATGTTGGTGGACGAGAGGCAGATCGAGCAATCGAGCAACAGT  TTCGCCCTCATGTTGGTGGACGAGAGGTAGATCGTCAGAGT  TTCGCCCTCATGTTGGTGAGAGGTAGAATCAGAGTAGAGTAGAGAGTAGAGTAGAGAGTAGAGAGTAGAGAGTAGAGTAGAGAGTAGAGAGTAG	CAGAAAGTCCAGGACCTCACAGAAGCTGAGGGAGGAGGAAGAAAAACTCAAAGCGTC TTTTTTTTTT	ACTTACAAATCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTCGAACAC  .::::::         :::         :::	1137GlualaThrCluThrLySGlnGInLeuasnserLeuargalaasnLeuGlu 1148 987 AAGGCCTCGAGGTTTTCCCAGGAGCACGAGGAGGAGGAGGCCAAATTGGCGAATCAAGAA 1046 :::	1149SerLeuGluLysGjüHisGjüAspLeuAlaAlaGlnLeüLysLysTyrGjü 1165 1047TCTCACAACCGGCAACTTCGACTCAAACTGGTTGGCTTATGGAAAGG 1094 :::::	1166 GluGinileAlaAsnLysGluArgGinTyrAsnGluGluIleSerGinLeuAsnAspGlu 118 1085 ATTGAGGAGTTGGAAGAGACTAATAAAAGGCTTTCAGAAGGGAAGGAA	

Alignment Scores:  Pred. No.: Score: Score: Score: Score: Pred. No.: Score: Sco	Oy 237 AAAAGCACCTCAAACCATCTGGAGAAAAGTGAGAAAAAGACT 278 :::::       :::	OY 279AAGAAGTCTGTGGAGTTATCCAAGAGGACCTCATCCAGCTCCTGAGTATCATGGAA 335	Qy 336 GGGGAGTTGCAGGAGGAAGATGTCATCCACATGCTGAGGACAGAAACCAAGCC 395	Oy 396 GAGGTTCTGGAGCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCAC 455 ::	Qy 456 CGAGATGCCATCCTTGATCAAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATC 515 :: :: :::       ::: ::: :: :: :: :: ::	OY 516 TCAGAGCTGGACAGACTGGAGGAAAAGCAGAGGAGGACGTACCGCCGCATGCTAGAGCAG 575	Qy 576 CTGCTGCTGGCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCAGGAGCAC 635	Qy 636 AAGCACTGACTACATGAACAAGAGC 662 ::	0y             663 GACGACTTCACCAACCTGCTGGAGAGGGGAGAGGGTTGAAAAAGGTCCTT 716               1036 GIUASpLeuSerSerArgLeuIleAspGluvaGGLuArgSerLysGlnLeuValLysala 1055               0y             717
1546	Oy 2091 GCAAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAACACCAAATGGCCAAGCACAAAGCC 2150  1605 ABHThrValLeuLy8SerLy8LeuGluAspIleGluArgGluLeuLy8AspLy8GlnAla 1624	Oy 2151 ATAGAGAAAGGGAGGCCGTGAGCCGAAGCCGAACTGCGACACAGGTTTCGGCTGAG 2210	Oy 2211 GAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGGTCTCAAGGAAGATCCACGAG 2270  Db 1637 ThrSerArgleuLysGluLeuGluGlnGluClaAspSerThrGlnGlnLysAlaGlnLys 1656	Oy 2271 CTGATGAACAAGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTC 2321	Qy 2322 CTTCAGCAAAGATTTATGGAAGAAACTAAGAACAAGAACATG 2366	Qy 2367 GGG	Qy 2379 CTCAATCTGACCAAGGAGCTATCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGT 2438	Oy 2439 GGGAACGCCGAAGGATGCTGGAC 2462  Db 1735 AenGluAspArgSerGluIleAsp 1742	RESULT 8  Tyling  Tyli

2022		1517 L			1557 L	2271 C			1596 A.		2414 -	1636 A			2439 G		2493 G		2529 CC			2613 GA	:: 1755 L)	2649 GC	1775 A	2709 CC		2769 C			
- č	8 8	qa —	ð 1	9 6	<b>3</b> 8	ờ	qq	<i>∂</i> #	9 8	. 음	ò	qa	ò	DP DP	δ	qa	ð í	<u>-</u>		3 8	<b>8</b> 8	ò	qq	ð	ପ୍ର	ð i	<u>a</u>	Š å		3 f	 _
1175 LeudluSerTyrLysGlnGluLeuGluGluSerAsnAspLysThrValLeuHisSerGln 1194 1020 ATGAACGCCAAATTGGCGAATCAAGAATTCACGGCGGCGGCGGCGCCAACTGAACTT GAACTTAAACTTAAACTT GAACTTCAAGATG 1076	LeuLysAlaLysArgAspGluGluTyrAlaHisLeuGlnLysGlnLeuGluGluGluThrVal	1077 GTTGGCTTTATCGCAAGGATTGAGAAGTGCAATAAAAGCCTTCAGAAG 1133 1215 LysSerSerGluGluValValGluGluWetLysAlaGlnAsnGlnLVaLVs1e1e11 1234		1235 LeuAsnGluThrIleAspGlnLeuLysArgGlnLysIleSerAlaAspLysAlaLysSer 1254	1173 AAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGGGCGTG 1232			1293 AAGAAGAGCTCCAAGAAGAACACCACAGAAGGAACTATAGACTAGAGTGGAGAAG 1352	1285 GluThrSerLeuMetGluLysAspHisLysMetArgGluMetGlnSerAsnLeuAspAsp 1304	1353 CTGCAGAAGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCG 1412		AlaAspGluThrLeuAsnSerAsnLeuLeuLysLysAsnAlaSerLeuAspMetGln	AGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGA	-::          1344	1530 CTGGAGAAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAGCTG 1574		1575 AAGTCCTTCACTGTGATGGTGGAGGAAAAATATGATGGAGAAAATAAAGCAA 1634	:::          ::::: 1373AlaValAlaValGluAlaArgAspAlaDaGlaCenAspAlaGlnGluLysIleGluLys 1391	1635 GAAGAGAGAAAGTGGATGGGTTGAATAAAACTTTAAGGTGGAGCAGGGAAAAGTCATG 1694	1392 GluvalLysGluvalLysGerLeuLeuAla 1401	GATGTGACGGAAAQCTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATG	GludladatgLysLeudspGluGludsnargGluValMetGluGluLeudrgLysLys	1/35   GMGGARAMGGAGGAGGAGGAGGGAGGAGGAGGAGGAGGAGGAGGAG	GAAGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGTT		ACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTC	1453 GluAlaGluAspValGlnLysGluLeu1461	1935 ACCTGCCCGGAAGACAATAAGATCAGAGAACTAACGCTTGAAATCGAGAGACTGAAG 1991	1462ThrAspValValAlaAlaThrArgGluMetGluArgLysMetArg 1476	1992 AAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGACTTGATGAAGACCGAGGACAATAT 2051	1477 LysPheAspGinGinLeuAlaGluGluArgAsnAsnThrLeuLeuAlaGlnGlnGluArg 1496
oy oy	QQ (	8 8	ò	q	કે ક	3 8	r q	ò	qq	કે ક	3 8	7 A	ò	qq	ò	o qq	ò	qq	ò	qq	ò i	<u>a</u> :	දු දු	à	අ	ò	Dp	ò	QQ	ò	qа

2052	GACCAGTIGGAGCAGAAGTICAGAACCGAGCAGGAIAAGGCAAACTICCTCTCCCAGCAG 2111
2112	CTCGAGGAAATCAAACACCAAATGGCCAAGCACAAAGGCATAGAGAAGGG 2162
2163	GAGGCCGTGAGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAG 2210
2211	. GAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAGAAGATCCACGAG 2270 :::
2271 1576	
2319	GTCCTTCAGCAAAGATTT :::::: AlaMetArgSerGluPheGl
2355	<b>£</b> \$
2414	
1636	AlaArgGlnAlaAlaIleAlaAsnLysLy
2415	TACAGCCGAGCT 243
1656	GluLysAsnGluAlaSerL
2439	GGGAACGGCCGAAGGATGGTGGACGTGC 
2493	GAGGCGGTGTGCGGGGAT
2529	CCGGCTGTTCATT
2562	
2613	GAACGG :::    LysArgArgLeuGl
2649	
2709	CCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGAG 276
1.81.1	1.92.1
2769	CTGGTCCTAGCACCAAAGCAGGCCAGCCCTACACATCCGTGTGACACCAGATCATGAG 2828
0	AACAGCACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTCTCTAGTACC 2888
1792	GlnMetThrAlaAspLeuAlaMetGluArgSerValCysGluArg 1806

3.48e-14 462.50 11y; 41.58% larity: 22.93% 2.98% (1-4364) y TOABOR	US-10-788-793-1 (1-4364) x T248U6 (1-1164)  QY 30 GGCGAAAGAACACCATTGGTTAAGGAGTCGACAACAGGTGGGAATGAGATCACGAAAT 89  H	130 OIYMEVAITHIAISOINEHEEGAGILEEGATULFALGIGSEISIYOHNOIHEETANSOIL 1. 90 CAAGGIGGAGAAAGTICAICTAACGGGCAIGICTCCTGCCCCAAGICCTCCAICAIC 14 176 Lenginginginyalixaginginaragixafienmeralaixaginmetserval 19	147AGCAGTGATGGTGGTAAGGCCCCTCAGAAGAAA 18	196 ThrMetArgGlulleThrAepGluSerGluSerGLyLyBvalGluMetGluAspLeuLys 21 186 AAGAACAAGGCCAATCGGAAGGAGGAGGAGGTCATGGCTTCCGGAACTATCAAAAGGCAC 24 :::	Db 216ArgGluLeuLyBValValLySSerAspValValArgTyrGlu 229 Qy 246 CTCAAACCATCTGGAGAAAGTGAGAAAAAGACTAAGAAGTCTGTGGAG 293	294 TTATCCAAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGG	Db 250 ValleuArgThrGluLeuValAenAlaGlnLysEuMetAspAlaIleSerGlnGluLys 269  Qy 339GAGTTGCAGGCTGGAGAAGATGCCACATGCTGAGGACAGAGAAAACCAAG 392  Dh 270 AenIlaGluIleIveGluHieIeuMaaGerIlaArgAanIcuSerMetGluArgGluIve 289	393 CCCGAGGTTCTGGAGGCACACTATGGATCTGCAGAACCTGAGAAA [	438		522CTGGACAGACAGGAAAAGCAGAAGGAGACGTACCGCCGCATGCTA 5.1	570	Qy         603 CGCACCCTGGAGAAC 626   <th>Qy 627 GAGAAGCACAAGCACACTGACTACATGAACAAGAGCGACGACTTC 671                                      </th> <th>Qy         672 ACCAACCTGCTGGAGCGAGAGAGGTTGAAAAAGCTCCTTGAA         719           10         11         12</th> <th>Qy 720 CAAGAAAAGCTTACCAAGCCCGCAAAAAAAGGGAAAACGCTAAGCGGCTCAAC 773 :::::: ::::                            </th>	Qy 627 GAGAAGCACAAGCACACTGACTACATGAACAAGAGCGACGACTTC 671	Qy         672 ACCAACCTGCTGGAGCGAGAGAGGTTGAAAAAGCTCCTTGAA         719           10         11         12	Qy 720 CAAGAAAAGCTTACCAAGCCCGCAAAAAAAGGGAAAACGCTAAGCGGCTCAAC 773 :::::: ::::
Qy 2889 ACCGTCATTCCTACCTTAGGCAACCAGAAACCAAGAATAACCATTATTCCATCACCCCAAT 2948  1807ThrGluSerAepLyslleAlaLeuGluArgAlaAsnArg 1819  Qy 2949 GTCATGTCGCAAAAGCCCAAAACTGCAGATCCTACTCTCGGCCCAGAACGAGCCATGTCC 3008  1820 AspLeuLysGlnGlnAspAlaGluAsn	Oy 3009 CCTGTCACGATTACTACTACTACTAGAGAAAGAGCCCGGAAGGTGGAAGGAGCCCTTT 3068	Qy 3069 GCCGACAGCCTGCATCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCACT 3128	Oy 3129 GAAATCGCTGTCTCTGGAATCTCAGGAAGTGCCTATGGGAAGGACTATC 3179	Qy 3180CTCAAAGTCACCCCGGAAAACTGTTCCAGCCCCCGTGCGGAAGTACAAC 3233	Qy 3234 TCCAATGCTAATATCACCACGGAAGACAATAAAATT	Qy 3273	Oy 3315 GCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAG 3374	Qy 3375 GAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGGAAC 3413	Qy 3414 CACCTCTCTAAGACCCGGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTC 3473	Qy 3474 ACAACGTCATCCACAGGAACCCAATCAGTGTCAGGACAAGTGGGTCATCTCAGGGG 3533  1977 AlaArgAapGlupheArgGlySerAlaLeuThrAanGlumetSerProSerAspArg 1995	Qy 3534 CCTACCCCCACCCGCATTCCTATGTCAAAGGTATGAAAGCTGCA 3578		C. Date: 15-Oct-1999 #Bequence_revision 15-Oct-1999 #text_cnange 15-Oct-1999 C. Accession: T24806 R. Burton, J. Surton, J. Submitted to the EMBL Data Library, October 1996	A;Reference number: 219937 A;Accession: T24806 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	A, Residues: 1-1164 <mil> A;Cross-references: EMBL:Z81118; PIDN:CAB03330.1; GSPDB:GN00023; CESP:T10G3.5 A;Experimental source: clone T10G3 C;Genetics:</mil>	A;Gene: CESP:T10G3.5 A;Map position: 5 A;Introns: 15/3; 73/3; 387/3; 412/3; 708/3; 818/3; 894/3; 982/3; 1080/2 Alignment Scores:

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Db 912LeuGluGluIleLeuHisAspLeuGluSerArgValGluGluGluGluGlu 928	QY 600 AGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACACACTGACTACATGAACAAG 659	Db 929 ArgaenGlnIeLeuGlnäenGluLysLysLysCluGlnGlyHieLysAenaep 946	Qy 660 AGCGACGACTTCACCAACCTGGAGCAGGAGGGGAGAGAGGTTGAAAAAGCTCCTTGAA 719		Qy 720 CAAGAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAACGCTAAGGGGCTCAACAAAACTT 779		では ネグネンフィン ネンネン イン 中国 プロロロ まで 田 アンファファ 田田 アファイ キャリロンフィン ネンギン カーギャン・アンド		9/6 GIUGIUGIUGINIIELIELEUGIUASPGINASNCYSLYSLEUALALYSGIULYSLYS	QY 840 CACATCGAGCAACTGGGGCCTGCAGAAAGTCCAGGACCTCACTCA	Db 995LeuleuGluAspArgileAlaGluPheThrThrAsnLeuThr 1008	Qy 900 GAGGAGGAAGAAAACTCAAAGGGTCACTTACAAATCCAAGGAAGACGCCCAGAAGCTG 959	Db 1009 GluGluGluLysSerLysSerLeualaLysLeuLysAsnLysHisGluAlaMet 1027	AGTTA	Db 1028 IleThrAspLeuGluGluArgLeuArgArgGluGluLysGlnArglnGlu 1044	CGCC	Db 1045 LeuGlulysThrArgArgLysLeuGluGlyAspSerThr 1057	Qy 1080 GGCTTATCGCAAAGGATTGAGGAGCTGGAAGAGACCAATAAAAGCCTT 1127		Qy 1128 CAGAAGGCAGAGGAAGAGCTCCAGGAGCTGAGAGAAAATTGCCAAAGGGGAATGTGGA 1187	Db 1078 AlaLysGluGluGluLeuGlnAlaAlaLeuAlaArgValGluGluGluAlaAlaGln 109	QY 1188 AACTCCAGTCTCATGGGGAAGTGGAGGGCGCAAGCGCGTGCTTGAGATGGAG 1244	Db 1098 LysAsnMetAlaLeuLysLysIleArgGluLeuGluSerGlnIleSerGluLeuGlnGlu 1117	Qy 1245GGC 1247	1118 AspLeuGluSerGluArgAlaSerArgAsnLysAlaGluLysGlnLysArgAspLeuGly	OY 1248 ANGGATUANGAANGACGAAGACGAAGAACGAAGAAGAAGAAGAAGAAGAAGAA	Qy 1284 CGGGAGCTGAAGAAGAAGCTCCAAGAAGAA 1313	   1158 GinGlübeuArgSerLysArgGlüGlüValAsnileLeuLysLysThrLeuGlüGlü	Qy 1314 GAACACCACCAGGAACTTAGACTAGAAGTGGAGAAGCTGCAGAAGAGGATGTCTGAG 1373	Db 1178 GluAlaLysThrHisGluAlaGlnIleGinGluMetArgGlnLysHisSerGlnAla 1196	1374 CTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTG :::::	1197 ValGluGluLeuAlaGluGlnLeuGluGlnThrLygArgLygValAla	Oy 1434 AACCTGGAGAAGGAGAAGAACCTAACCAAGGACTGCTGCTGACGACTG 1481 	Qy 1482 GAGGTGGTCAAGAGTCGA 1499	Db 1233 LysValLeuLeuGlnGlyGlyArgAspSerGluHisLysArgLysLysValGluAlaGln 1252
UD 1131 YLYBHIETYTCYBASHFTOCVBSSETSBTLYB 1141	RESULT 10	myosin heavy chain, neuronal [similarity] - rat	N;Contains: myosin ATPase (EC 3.6.4.1)	C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002	C;Accession: Silvin; FNUO13; Sili34 R;Sun, W.; Chantler, P.D.	a neuronal my	856; PMID:1569576	A; Molecule type: mRNA	A;Cross-references: EMBL:X62659	R;Sun, W.; Chantler, P.D. Biochem. Biophys. Res. Commun. 175, 244-249, 1991	A;Title: A unique cellular myosin II exhibiting differential expression in the cerebral A;Reference number: PN0013; MUID:91151356; PMID:1998509	A; Accession: PN0013 A:Molecule rone: mRNA	A; Residues: 1914-1998, 'I' <su2></su2>	Artagerimental Bource: Diain C.Superfamily: myosin heavy chain; myosin motor domain homology C.Kowarde: artin binding: 200: roiled roil: bydroless: methyleted emino erid: munlastid	string, military cont	F.51-575/Region: actin binding #stedicted 5.521-675/Region: actin binding #stedicted 5.521-675/Region: actin binding #stedicted	F;835-1999/Domain: coiled coil #status predicted <coi></coi>	F;836-1276/Region: S2 F;1277-1999/Region: light meromyosin	, R (1, N	F1959, Nos/Active site: Cys #status predicted F1916/Binding site: phosphate (Ser) (covalent) #status predicted F1943/Binding site: phosphate (Ser) (covalent) #status predicted			ercent Similarity: 42.77% Conservative: est Local Similarity: 24.28% Mismatches:	5.97%	US-10-788-793-1 (1-4364) x S21801 (1-1999)	273 AAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATCATG		Qy         333 GAAGGGAAGTTGCAAGGTCGAGAAGATGTCATCCACATGCTGAGGACAGAAAACC 389           Dh	390 AAGCCCGAAGGTTCTCGCAAGGAACACTTTGGAATCTAAGGAAACCTAAAAAAAA	862 LW8ValGlu	GTCCTGCACGAGATGCCATCCTTGCTCAAGAAGAAGTCCATAGGAGAAGAC		498	894 LeuPheAlaGluAlaGluGluMetArgAlaArgLeuAlaAlaLysLysGlnGlu	Qy 558 CGCCGCATGCTAGAGCAGCTGCTG

Qy         2355 AACAAGAACATGGGAGGGAGGTCCTCAATCTGACCAAGGAGTCTTTCCAAG         2411           Db         1584 GlnLysLysLeuvalArgGlnValArgGluMetGluAlaGluLeuGluAspGlnArgLys         1603           Qy         2412 CGCTACAGCCGAGCT         2426           Db         1604 GluMetBerArgAla         1608	RESULT 11 A40997 myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians) N;Contains: myosin ATPase (EC 3.6.4.1)	C;Species: Aequipecten irradians C;Decies: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Apr-2002 C;Accession: A40997; S13557 R;Nyitray, L.; Goodwin, E.B.; Szent-Gyoergyi, A.G.	J. Biol. Chem. 266, 18469-18476, 1991 A,Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Sequ. A,Reference number: A40997, MUID:92011595; PMID:1917970 A,Rocession: A40997	A;Molecule type: mkNIs A;Residues 1-1938 «NYI» A;Cross-references: GB:X55714; NID:g5611; PIDN:CAA39247.1; PID:g5612 C;Superfamily: myosin heavy chain; myosin motor domain homology	C; keywords: actin Dinding; ATF; colled coll; hydrolase; muscle contraction; nucleotide bi F;86-763/Domain: myosin motor domain homology <mmot> F;176-183/Region: nucleotide-binding motif A (P-loop) F;176-186/Region: actin binding #status predicted</mmot>	F:653-675/Region: actin binding #status predicted F:836-1938/Domain: coiled coil #status predicted <coi> F:836-1276/Region: S2 F:1277-1938/Region: light meromyosin</coi>	F;182/Binding Bice: ATP (Lys) #status predicted F;693,703/Active site: Cys #status predicted Alignment Scores:	6.63e-14 457.00 1arity: 43.06% imllarity: 22.54%	Udery Macch: 5.91* Indels: 187 DB: (2-10-788-793-1 (1-4364) x A40997 (1-1938)	Qy 71 GGGAATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCATGTCTCCTGCCC 130	Qy 131 CAAGTCCTCCATCATCAGCAGTGATGGTGGTAGGGCCCCTCAGAAGATGCAAAAAGAA 190        :::	Qy       191 CAAGGCCAATGGAAGGAGGAGGATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAA       250         Db       187 uSerlleAlaArgGlnGluGluGlu	Qy 251 ACCATCTGGAGAAAAAAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGCT 310	Qy     311 CATCCAGCTCCTGAGTATCATGGAGGGGAGTTGCAGGCTCGAGAAGATGTCATCCACAT     370       Db     871 uGluGlnAsnValThrLeuLeuGluGlnLysAsnAspLeuPheLeuGl     887	OY 371 GCTGAGGACAGAGAAAACCGAGGCTCTGGAGGCACACTATGGATCTGCAGAACC 430	Oy 431 TGAGAAAGTGCTTCGGGTCCTGCACGAAGGCCTTGCTTGC
Oy         1500 GTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGTTAAGCCTCAAAGAT 1559           Db         1253 LeuGlnGluLeuGlnValLysPheAsnGluGlyGluArgArgValThrGluLeuAlaAsp 1272           Oy         1560 GACCTTACAAGCTGAAGTCCTTCACTGTGATGCTGGATGAGAGAAATATGATG 1619           Db         1273 LysValThrLysPheuGlnValGluLeuAspAsnValThr 1285	GGAAAGTGGATGGGTTGAATAAAACTTTAAGGTGGAG 	1680 CAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAA 1739 11. 11. 11.	1740 CTGAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGGAGGGATGAGCTGATG 1799     ::::::::::	Qy 1800 GGTAAACTGAGGAGCGAAGAACAAAGCTCCTGTGAA 1835 	Qy 1836 CTGAGCTGCAGTGTACTTACTAAAGAAGCGG	Qy 1875 GGCATAGAGGAGATAGAAATAAACCGAGGTAGGTCGTGCAAGGG 1925 	Qy 1926 TCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGAACTAACGCTTGAAATCGAGAGA 1985	GGAGGTGGT  ::: uAspAspLeuLeuVa	2028 TTGATGAAGACCGAGGACGAATATGACCAGTTG 2060	2061	2097 TTCCTCTCCCAGCAGCAGAAATCAAACACCAAATGGCCAAGCACAAAGCCATAGAG 2156 	2157 AAAGGGAGGCCGTGAGCAAGAAGCCGAACTGCGACACAGGTTT 2201       ::       1487GlualaMetGluGlnLysAlaGluPheLeuArgLysAsnLeuGlnGluMetThr 1504	2202CGGCTGGAGGACTAAAAGTCCT	2226GATTTACAGGCCGAGGTGCAGGCTCTCAAGGAGAAGATCCACGAGCTGATGAAC 2279	2280 AAGGAAGACCAGCTGTCTCAG	2319 GTCCTTCAGCAAAGATTTATG

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:::|||||||||:: 1266 rIleAsnGluLeuGlnSerGlnLysSerArgLeuGlnAlaGluAsnSerAspLeuThrAr 1286 AGAACTCGAATGCTCCGAGAGTAGACTG-----GAGAAGGCCGAGTTAAG 1549 C-----CTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGA 1603 GAGGGATGAG------CTGATGGGTAAACTGAGGGGGAAGAAGAAAGGTCCTG 1831 :::|||::::: 1421 uLeuGluAspMetSerIleGluValAspArgAlaAsnAlaSerValAsnGlnMetGluLy 1441 -------TCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGAACTAAC 1969 2017 2128 2179 |:::::: ||| ::: sGluLeuAspLysAlaArgArgLeuGluMetGluLysGluGluLeuGlnAlaAlaLe 1541 2347 1664 AAACTTTAAGGTGGAGCAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAG 1723 |||| ::: |1401 rGluAlaAlaAsnAlaLysCysSerAlaLeuGluLysAlaLysSerArgLeuGlnGlnGl 1421 2018 GGAGGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAAC 2077 -----Se 1266 AACTAAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCTAGAGCTTTC 2407 ::::|||||| :::::||| | ||| ::: gGlnLeuGluAspAlaGluHisArgValSerValLeuSerLysGluLysSerGlnLeuSe GAGGAAAAATATGATGGAGAAAATAAAGCAAGAAGAGGAAAGTGGATGGGTTGAATAA : ::::: ::: ::: ||||::: ||| ::|| nAsnGluIleGlnTrpArgSerLysPheGluSerGluGlyAlaAsnArgThrGluGl |||| ::: ::: ::: ::: ::: ||| ::: ::: || | ::: ::: || | ::: ::: aArgSerLysLeuGlnAsnGluValArgAsnMetHisAlaAspAhalleArgGl CAAGAAGCTTTTAAAACTCAAAATCTGAAAAGGAAAAAGGAGTACAGTCTGACAAAGGA 1970 GCTTGAAATCGAGAGCTGAAGAACGGCTCCAG------CAGTTGGAGGTGGT ---ATCAAACA CCAAATGGCCAAGCACAAA------GCCATAGAGAAAGGGGAGGCCGTGAGCCAGGA GGTGCAGGCTCTCAAGGAGAAGATCCACGAG----CTGATGAACAAGGAAGACCAGCTGTC TGAACTGAGC-----TGCAGT---GTAGACTTACTAAAGAAGCGGCTT---GATGG CATAGAGGAGGTAGAAAGGGAAATAAACCGAGGTAGGTCGTGCAAGGGG-------2180 AGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGA 1541 uGludluAlaGluGlyAlaLeuGluGlnGlüdlüAlaLyeValMetArgAlaGlüLeuGl TCAGCTCCAAGTCGACTATTCG------GTCCTTCAGCAAGATTTATGGAAGAGA |||::: ::: |||::: nLeuAlaAspGluIleHisAspLeuThrHi 2078 CGAGCAGGATAAGGCAAACTTCCTCTCCCAGCAGCTCGAGGAA----

101 AAGTICATCTAACGGGCATGTTCCTCCCCCAAGTCCTCCATCATCACGAGGTGATGTTGGT   16	1107 uGlnAlaAlaLeuAlaArgGlyAspGluGluValLeuGlnLysSnAsnAsnThrLeuLysLe 1127 1076 GGTTGGCTTATCGCAAAGGATTGAGGAGGAGAAGAGACCAATAA 1120 1127 uValArgGluLeuGlnAlaGlnIleAlaGluLeuGlnGluAspLeuGluSerGluLysAl 1147
5	90 60 60
CGGCCTCCAGGCGCAAA ValalaleNapalaMethrgile ValalaleNapalaSerAsnArg GGGGTCTCAGGCGGGGGGGGGGGGGGGGGGGGGGGGGGG	t Similarity: ocal Similarity: Match: 788-793-1 (1-4364)

:::	Qy         2303 CCAAGTCGACTATTCGGTCCTTCAGCAAGATT           b         1550 gAlaLeuAspGlnGlnValGluMetArgTh           Qy         2363 CATGGGAGGAGGTCCTCAATCTCACCAAGGA           Qy         2414 CTACAGCGAGGGTCCTCAAGTCTCACCAAGGA           Qy         2414 CTACAGCCGAGCTCTCAGGCCGAGTGGGAACGG           Pb         1590 nPheGluArgAspLeuGlnThrArgAspGluGln           Qy         2474 CTCCACTGGGGTGCAGCGAGTGGGAACGG           Qy         2474 CTCCACTGGGGTGCAGACCGAGGCGGTGGGG           Qy         2474 CTCCACTGGGGTGCAGACCGAGGCGGTGCGGG           Db         1610 lLygGlnValArgGluLeuGluAlaGluLeuGlu           Qy         2534 TGTGTTCATTCGCAAATCCTTCCAG 2558	Db 1630 aValAlaileLysbyBLysbeudiu 1638 RESULT 13 A4336 microtubule-vesicle linker CLIP-170 - human C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1; C;Accession: A4336 R;Pierre, P.; Scheel, J.; Rickard, J.E.; Kreis, Cell 70, 887-900, 1992 A;Title: CIIP-170 links endocytic vesicles to m: A;Reference number: A4336; MUID:92405160; PMID A;Accession: A4336 A;Actus: preliminary A;Molecule type: mRNA A;Residues: 1-1392 <pie> A;Cross-references: GB:M97501; NID:g180621; PIDI</pie>	Alignment Scores:
121 AAGCCTTCAGAAGGAAGACTCCAGGAGCTGAGAAAATTGCCAAAGGGGA   1180	GCAGAAGAGGATGTCTGAGGAAGCTGGAGGAGGCGTCACCCGGAGTAAGTCGGA		CAGTGTAGACTTACTAAAGAAGCGGCTTGAT
8 8 8 8 8 8 8	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	6 8 6 8 6 8 6 8 6

SCTAAAAGTCGTGATTTACAGGCCGAGGT 2242 |||:: |||:: ||aGluMetGluAspLeuMetSerSerLy 1535 ::: |InAenGluGluLysLysArgAlaLeuVa 1610 rgAspArgAlaGluAlaAspAlaArgGl 1495 SCCGTGAGCCAGGAAGCCGAACTGCGACA 2194 |||::: ::: ||aLeuAspGluAlaLeuGluAlaGlnAs 1515 TGAACAAGGAAGACCAGCTGTCTCAGCT 2302 ::: |||::: -------GluLy8SerLy8Ar 1550 AGCTAGAG------CTTTCCAAGCG 2413 ||::: |luValAsnMetGlnAlaMetLysAlaGl 1590 GCCGAAGGATGGTGGACGTGCCTGTGGC 2473 GGGATGCTGCGGAGGAGGACCCCGGC 2533 |||| | iluAspGluArgLysGlnArgAlaMetAl 1630 GTCTGTGGAGTTATCCAAGGAGGACCTC 311 AAAAGAAGGCCAATCGGAAGGAGGAG 212 ::|||::::: !uLysSerArglleMetGluLeuGluLys 471 CTATCAAAAGGCACCTC-----AAA 251
:::::||| ||| |||
LuLeuArgArgArgLeuGluSerAsnLy8 491 1993 #text\_change 05-Nov-1999 :DN:AAA35693.1; PID:g180622 microtubules. ID:1356075 s: vative: ches: ', T.E.

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956 GACGICTATGAGAAACCTATCTCAGACCACACACCAGAGAAAAACCAAAAGAAACCTATGAGAAACCTATCTCAGACCACACACA	1072 AlaAspLeuGlnÄlädinijeÄläGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAA 1109 1074 CTG
6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8	3 B 3 B 3 B 3 B 3 B 3 B 3 B 3 B 3 B 3 B
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MEDLINE=95096166; PubMed=7798308;

Byrd D.A., Swell D.J., Pante N., Konstantinov K.N., Guan T.,

Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.;

"Tpr, a large coiled coil protein whose amino terminus is involved in activation of encogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";

J. Cell Biol. 127:1515-1526(1994).
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"The human tpr gene encodes a protein of 2094 amino acide that has
"The human tpr gene encodes and an acidic C-terminal domain.";
Oncogene 7:2329-2333(1992).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Nucleoprotein TPR.
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-DG=/cgn1 / USEPO bool _D/USIO798193/runat 07092004 134020 10801/app_query.fasta_1.4551
-DB=SwissProt_42 -QFWT=fastan -SUFFIX=rsp_-MINMATCH=0.1 -LGOPEL=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosume2 -TRANS=human40.cdi -LLST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWM=pcb -NORM=ext -HEAPSIZE=500 -MINNEN=0 -MAXIEN=200000000
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CC -1- TISSUE SPECIFICITY: Highest in testis, lung, thymus, spleen and brain, lower levels in heart, liver and kidney.  CC -1- DISEASE: Involved in tumorigenic rearrangements with the MET, TRK or RAF genes.  CC -1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;  WWW=http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html".  CC This SWISS-PROT entry is copyright. It is produced through a collaboration companies the Swiss Institute of Bioinformatics and the EWBL outstation.  CC This SWISS Institute of Bioinformatics and the EWBL outstation composite institutions as long as its content is in no way compatities requires a license agreement (See http://www.isb-sib.ch/announce/corrected and email to license@isb-sib.ch).	DR GENEW, 70067212017; PR.  DR GORNEW, 70067212017; PR.  DR GO, 6001005737; C:Cytoplasm; TAS.  DR GO, 6001005737; C:Cytoplasm; TAS.  DR GO, GO:0005643; C:nuclear pore; TAS.  DR GO, GO:0005640; P:Dotoconcogene, Chromosomal translocation;  KW Coiled coil; Proto-oncogene, Chromosomal translocation;  KW Coiled coil; Protoconcogene, Colled Coil (POTENTIAL).  FT DOMAIN 1788 805 COILED COIL (POTENTIAL).  FT DOMAIN 834 869 COILED COIL (POTENTIAL).  FT DOMAIN 1136 1166 COILED COIL (POTENTIAL).  FT DOMAIN 1136 1166 COILED COIL (POTENTIAL).  FT DOMAIN 1262 1304 COILED COIL (POTENTIAL).  FT DOMAIN 1262 1304 COILED COIL (POTENTIAL).  FT DOMAIN 1264 1304 COILED COIL (POTENTIAL).  FT DOMAIN 1267 1304 POLY-SER.  FT DOMAIN 1267 1304 POLY-SER.  FT DOMAIN 1267 1304 POLY-SER.  FT DOMAIN 1366 1595 2298 POLY-SER.  FT DOMAIN 1367 1364 POLY-SER.  SQ SEQUENCE 2349 AA; 265600 MW; AFDD685CEDCA9EF CRC64;  Alignment Scores: 1.57e-12 Length: 2349  DOMAIN 1604 1604 Matches: 2104 POLY-SER.  Best Local Similarity: 36.85\$ Conservative: 252  Best Local Similarity: 1606 164 Mismatches: 510  Ouery Match: 1606 1606 1606 1606 1606 1606 1606 160	US-10-788-793-1 (1-4364) x TPR_HUMAN (1-2349)

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1687 AlaGlyAsnLysSerThrProArgAlaSerIleArgPro---------MetValThr 1702
 ---GATCATGAGAACAGCACTGCCACC 2843
                            1649 ThrThrProAlaSerGlyGluArgGlyIleAlaSerThrSerAspProProThrAlaAsn 1668
                                                                                                                            2961 AAGCCCAAAAGTGCAGATCCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATT 3020
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1835 GluGluAspSerThrIleGluAlaSerAspGlnValSerAspAspThrValGluMetPro 1854
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1875 GluSerThrAspGlyGluValGluThrGlnValTyrAsnGlnAspSerGlnAspSerIle 1894
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                                                                                        1669 IleLysProThrProValValSerThrPro----SerLysValThrAlaAlaAlaMet
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CENE\_HUMAN STANDARD; 1D CENE\_HUMAN STANDARD; AC 002224; DT 01-JUL-1993 (Rel. 26, Created)

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CHARACTERIZATION.
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MEDLINE=98437347; PubMed=9763420;
Chan G.K.T., Schaar B.T., Yen T.J.;
J. Cell Biol. 143:49-63(1998).
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                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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10-OCT-2003 (Rel. 42, Last annotation update)
Centromeric protein E (CENP-E protein).
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Mammalia, Butheria, Primates;
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EMBO J. 14:918-926(1995).
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Genew; HGNC:1856; CENPE.
GK; Q02224; --
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DR PROSITE; PSS0067; KINESIN MOTOR DOMAIN2; 1.  KW MOTOR protein; Cell division; ATP-binding; Coiled coil; Mitosis;  KW Cell cycle; Centromere; Lipoprotein; Prenylation.  FT DOMAIN 3156 2471 COLLED COIL (POTENTIAL).  FT DOMAIN 2472 2663 GLOSBULAR (POTENTIAL).  FT DOMAIN 86 93 ATP (BY SIMILARITY).  FT NP BIND 86 93 ATP (BY SIMILARITY).  FT LIFID 2660 2660 S-farnesyl cysteine.  SQ SEQUENCE 2663 AA; 312087 MM; CEFC13880C8C8CBB CRC64;	8: 1.98e-12 473.50 1ty: 39.37% larity: 20.61% 1.4364	OS-10-793-1 (1-4304) X CENE_HUMAN (1-2803)  OY 171 TCACAAGATGCAAAAAAGACCAATCGGAAGGAGGAGGAGT	Qy 216	Oy 249 AAACCATCTGGAGAAAGTGAGAAAAAGGAGTCTGTGGAG 293  :::	Qy     294 TTATCCAAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGAGGTTGCAGGCT 350       Db     1442 LysGluLysAspAspLeuGlnArgLeuGlnGluValLeuGlnSerGluSerAspGlnLeu 1461	Oy 351 CGAGAAGATGTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAG 407 :::   :::   :::   :::  Db 1462 LysGluAsnIleLysGluIleValAlaLysHisLeuGluThrGluGluInGluLeuLysVal 1481	Oy 408 GCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATC 467	Qy       468 CTTGCTCAAGAGACCTAAGAGACGTCTATGAGAAACCTATCTCAGAGCTG 524	Oy 525 GACAGACTGGAGGAAAGCAGAGAGAGACGTACCGCATGCTAGAGCAGCTGCTGCTG 584		603 CGCACCGTGTACGAGCTGGAGAACGAGAAGGACAAGCACACCTGACTAC 6 1::	ATGAACAAGAGGGGGGGCTTCACCAACCTGGAGGAGGAGGAGGAGGAGGTTGAAAAAG 7	Oy 711 CTCCTTGAACAAAAAGCTTACCAAGCCGGCAAAGAAAAGGAAAAGGCTAAG 764 :::::::	CAACAAACTTCGAGATGAGCTTGTGAAGCTCAAGTCCTTC 	810 GCCTCATGTTGGTGGACGAGAGGCAGATGCACATCGAGCAACTGGGCCTGCAG

GCAGAAGAAGGATGTCTGAGCTGGAGAAGCTG 1385 ||||| ||| :::::||| |Thr---LysGluArgAspAspLeuArgSer 1693 GAACGCCAAATTGGCGAATCAAGAATCTCAC 1052 : :: ||| uLyslleValHisMetHisLeuLysGluHis 1733 |::: |||::::;; yIleValSerGluLygThrAsnGluIleSer 1752 GGAAGAGCTCCAG------GAGCTG 1157 sleulysGluGlnGlnGluThrlleAspLys 1792 CAAG-----GATGAAGAGATCACG 1265 GAAGAAGCTCCAAGAGGAAGACACCACAGC 1325 :::::|||::: eGlnGluLeuLysAlaAsnGluHisGlnLeu 1832 : |||||| ||| rLeuSerLysLeuGlulleGluAsnLeu--- 1871 CAAAGACCTGCTGAACGAGCTGGAGGTGGTC 1490 |||||| ||| sGluIleGluHisLeuLysGluGlnPheGlu 1654 pGlnLeuLysGluAsnLeuArgGluThrIle 1713 CTTA---TCGCAAAGGATTGAGGAGCTGGAA 1109 AAACTCCAGTCTCATGGCGGAAGTGGAGAGT 1217 CCGCAGTAAGTCGGAATGCACCCAGCTCCAT 1430 :::::||| ::: aGlnGluLeuHisGluAsnLeuGluGluMet 1884 CGAATGCTCCGAGAGTAGACTGGAGAAGGCC 1541 GCTGAAGTCCTTCACTGTGATGCTGGTGGAT 1601 : |||::: uThrLysAlaArgAspLeuGluIleGlnGln 1924 GCAAGAAGAGGAAAGTGGATGGGTTGAAT 1661 |::: ::: |||||| sGluHisLysGluThrValAspLysLeuArg 1944 CATGGATGTGACGGAAAGCTAATCGAGGAA 1721 : ::: ||| :::::: ::: eSerGluLysThr1leGln1leSerAsp1le 1957 AATGGAGGAAAAGGAGTACAGTCTGACAAAG 1781 |:::::::::||| uLeuGlnLysLysIleGlnGluLeuGlnLys 1977 GAGCGAAGAAGGTCCTGTGAACTGAGC 1841 CACTTACAAATCCAAGGAAGACCGC----- 950 ------GACCTCACTCAGAAGCTG 896 C----TTCGAACACAGGCC 992

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SUDGENCE TRYAN N.A.

RAY MEDLINE-20057165; PubMed=10591208;

RAY Dunham I. Hunt A.R. Colling J.E., Barese K.N., Beabage A.K.,

Clamp M., Smink L.J., Anaccough R., Almeida J.P., Bubbage A.K.,

RAY Clamp M., Smink L.J., Barlow K.F., Barese K.N., Beabagey O.P.,

RAY Clamp M., Smink L.J., Barlow K.F., Barese K.N., Beabages J.,

RAY CLOSPY S.M., Carder C., Carter N.P., Chen Y., Clark G.,

Conroy D., Corby N.R., Coville G.G., Cox A.V., Davis J., Dawson E.,

RAY Dami. P.D. Dockere C., Doddworth S.J., Durbin R.M., Ellington A.G.,

RAY Conroy D., Corby N.R., Coville G.G., Cox A.V., Davis J., Dawson E.,

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RAY Hall R.E., Hall-Tamlyn G., Heathcott R.W., Hos S., Hollmes S.,

Hunt S.E., Jones M.C., Rerebaw J., Kimberley A.M., King A.,

Hall R.E., Jones M.C., Everein M., Matthews L.H., Moccann O.T.,

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RAY Sodderlund C., Spragon L., Steward C.B., Sultern J.E., Swann R.M.,

RAY Milliams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RAY Sodderlund C., Spragod L., Steward C.B., Sultern J.S., Smith M.,

RAY S., Chen F., Chu L., Crabtree J. M., Milliams S.,

RAY RAWSON W. Wall M., Wall M., Wall M., Yoo Z.,

RAY Shinman A., Shibuya K., Hub A., Kenton S., Lai H., Lao H.I.,

RAY Mang O., Wang Y., Wang Z., Williamson D., Bentley D., Beadalbaw H., Bourne S.,

Coddell J.A., Hillier L., Wohlaum D., Ozersky P., Rohling T.,

RAY Milson R., Johnson D., Bentley D., Walley R., Warterston R.,

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                                                                           2614 euProSerbroHisProValArgTyrPheAspAsnSerSerLeuGlyLeuCysProGluV
                                                          ----AGCTGGAAAGCCAGTAGTG
                                                                                                                                                                                                 MYH9 HUMAN STANDARD; PRT; 1960 AA.
135579; 060805;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
17-MAR-2014 (Rel. 43, Last annotation update)
18-MAR-2014 (Rel. 43, Last annotation update)
18-MAR-2014 (Nonmuscle myosin heavy chain, MYH9.
                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
3531 CGGCCTACCCCCACCCGCATTCCTATGTCAAAAGGTATGAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of human chromosome 22.";
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"The DNA sequence of hum
Nature 402:489-495(1999)
                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                GC 3592
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MEDLIKE=20428192; PubMed=10973259;
Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C.,
Seri M., Cusano M., Gangarossa S., Caridi G., Bordo D., Lo Nigro C.,
Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito M.,
Iolascon A., Zelante L.L., Savoia A., Balduini C.L., Noris P.,
Magrini U., Belletti S., Heath K.E., Babcock M., Glucksman M.J.,
Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.;
"Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human nonsyndromic hereditary deafness DFNA17 is due to a mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lalwani A.K., Goldstein J.A., Kelley M.J., Luxford W., Castelein C.M.,
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-1-DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
-1-DISEASE: Defects in MYH9 are the cause of May-Hegglin anomaly (MHA) [MIM:155100]. MHA is an autosomal dominant macrothrombocytopenia characterized by thrombocytopenia, giant
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DISEASE: Defects in MYH9 are the cause of Fechtner syndrome (FTNS) [MIM:153640]. FTNS is an autosomal dominant macrothrombocytopenia characterized by thrombocytopenia, giant platelets and leukocyte inclusions. With additional alport-like clinical features of sensorinneural deafness, cataracts and nephritis.

DISEASE: Defects in MYH9 are the Common syndrome (SBS) [MIM:605249]. SBS is an autosomal dominant macrothrombocytopenia characterized by thrombocytopenia, giant platelets and leukocyte
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-715 FROM N.A.
MEDILINE=91316803; PubMed=1860190;
Simons M., Wang M., Wabride O.W., Kawamoto S., Yamakawa K.,
Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains are encoded by two genes located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20428193; PubMed=10973260; Kelley M.J., Jawien W., Ortel T.L., Korczak J.F.; "Mutation of MYH9, encoding non-muscle myosin heavy chain A, in May-Hegglin anomally."; May-Hegglin anomally."; Mat. Genet. 26.106-108(2000).
-i- FUNCTION: Cellular myosin appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and
                            MEDLINE=92003925; PubMed=1912569;
Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M., Arnaout M.A., Claycon L.K., Tenen D.G.;
"Cellular myosin heavy chain in human leukocytes: isolation of 5'
cDNA clones, characterization of the protein, chromosomal
localization, and upregulation during myeloid differentiation.";
Blood 78:1826-1833(1991).
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"Human nonmuscle myosin heavy chain mRNA: generation of diversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    through alternative polyadenylylation.";
Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
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MEDLINE=20489856; PubMed=11023810;
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MEDLINE=90138958; PubMed=1967836;
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Nat. Genet. 26:103-105(2000).
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SEQUENCE OF 1-1337 FROM N.A.
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                                                                                            This SWISS-ROOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSS0096; IQ; 1.

PROSITE; PSS0096; IQ; 1.

Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil; Multigene family; Disease mutation; Deafness.

DOMAIN

MYOSIN HEAD-LIKE.
nonsyndromic sensorineural deafness 17 (DFNA17) [MIM:603622]. DFNA17 is characterized by progressive hearing impairment and cochleosaccular degeneration. SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R -> C (IN SBS).
FTIG-VAR 010795.
D -> H (IN FTNS).
FTIG-VAR 010796.
FTIG-VAR 010797.
FTIG-VAR 010797.
RAI -> RGH (IN REF 3).
T -> M (IN REF 3).
T -> M (IN REF 4).
C -> Y (IN REF 4).
KG -> GR (IN REF 4).
KG -> GR (IN REF 4).
E -> EE (IN REF 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1Q.
COLLED COIL (POTENTIAL)
ATP (POTENTIAL).
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | N -> K (IN MHA) | N -> K (IN MHA) | N -> K (IN MHA) | N -> K (IN FUNS) | PTIC=VAR 010792 | N -> H (IN DEVALT) | PTIC=VAR 010793 | N -> I (IN MHA) | N -> I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / FTIG=VAR 010794.
                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 155100; ...
MIM; 135400; ...
MIM; 6036240; ...
MIM; 603622; ...
GO; GO:00005660; C:non-muscle myosin; TAS.
InterPro; IPR001009; myosin_Nosin_LerPro; IPR001009; myosin_Lead.
InterPro; IPR001009; myosin_Lead.
InterPro; IPR002298; Myosin_Lail.
InterPro; IPR0022017; Spectrin.
                                                                                                                                                                                                                                                                        EMBL; 282215; -; NOT ANNOTATED_CDS.
BRBL; MBLIOS; AAAA59888.1; -
EMBL; MG9180; AAAG1765.1; -.
EMBL; M1013; AAA36349.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00612; 10; 1.
Pfam; PF0065; myosin head; 1.
Pfam; PF02736; Myosin N; 1.
Pfam; PF01576; Myosin Lall; 1.
PRINTS; PR00193; MYOSINHEAVY.
SMART; SM00015; 10; 1.
SMART; SM00015; 10; 1.
                                                                                                                                                                                                                                                                                                                                               PIR; A61231; A61231.
HSSP; P10587; 1BR2.
Genew; HGNC: 7579; MXH9.
MIM; 160775; -.
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Pred. No.:
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VARIANT
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Length: Matches: Conservative:

Score: Percent Similarity:

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1053 LeuGluGlyAspSerThrAspLeuSerAspGlnIleAlaGluLeuGlnAlaGlnIleAla 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           984 GluAspGlnAsnCysLysLeuAlaLysGluLysLysLeuLeuGluAspArgIleAlaGlu 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           942 GAAGACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACAAAGGCCTCGAGGTTT 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002 TCCCAGGAGCACGAAGAGATGAACGCCAAATTGGCGAATCAAGAATCTCACAACCGGCAA 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1062 CTTCGACTCAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAA------ 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1170 GCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGC 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1093 GluGluGluAlaAlaGlnLysAsnMetAlaLeuLysLysIleArgGluLeuGluSerGln 1112
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|1153 AspSerThrAlaAlaGlnGluLeuArgSerLysArgGluGlnGluValAsnIleLeu 1172
                                                                                                                                                                                                              845 GluGluMetMetAlaLysGluGluGluLeuValLys---ValArgGluLysGlnLeuAla 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                    639 CACACTGACTACATGAACAAGGGGGAC-------GACTTCACCAACCTG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681 CTGGAGCAGAGCGAGAGGTTGAAAAAGCTCCTTGAACAAGAAAAAGCTTACCAAGCC 740
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                                                                                                                                                                                                                                                                                                                                                                                                            579 CTGCTGGCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904 AlaArgLeuThrAlaLysLysGlnGluLeuGluGluIleCysHisAspLeuGluAlaArg 923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              768 CTCAACAAACTTCGAGATGAG-----CTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               822 GTGGACGAGAGGCAGATGCACATCGAGCAACTGGGCCTGCAGAGGTCAGAAAGTCCAGGAC 881
                                                                                                                                                                             459 GATGCCATCCTTGCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCA
                                                                                                                                                                                                                                                                                           519 GAGCTGGACAGACTGGAGGAAAAGCAGAAGGAGACGTACCGCCGCATGCTAGAGCAGCTG
                                                                                                                                                                                                                                                                                                                                   1230 GTGCTTGAGATGGAG-----
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                                 Indels:
                                                                                                                 US-10-788-793-1 (1-4364) x MYH9_HUMAN (1-1960)
Best Local Similarity: 23.21%
Query Match: 6.07%
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1055 GlnIleSerLeuLeuLysGluLysLeu-----GluThrAlaThrThrAlaAsnAspGlu 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988 Ser------LysAsnGluSerSerTleGlnLeuSerAsnLeuGlnAsnLysIllasp 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1005 SerMetSerGlnGluLysGluAsnPheGlnIleGluArgGlySerIleGluLysAsnIle 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1047 ------TCTCACAACCGGCAACTTCGACTCGAACTGGTTGGCTTATCGCAAAGG 1094
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                                 AAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     750 AAGGAAAAC---GCTAAGCGCTCAACAACTTCGAGATGAGCTTGTGAAGCTCAAGTCC 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          807 TTCGCCCTCATGTTGGTGGACGAGAGGCAGATGCACATCGAGCAACTGGGCCTGCAGAGT 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    927 ACTTACAAATCCAAGGAAGACGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACAC 986
                                                                                                                                                                           968 AlaAsnAsnTyrLysAspMetGlnAlaGluAsnGluSerLeulleLysAlaValGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 GAGCTGGACAGACTGGAGGAAAAG------CAGAAGGAGACGTACCGCCGCATGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   570 GAGCAGCTGCTGCTGGCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAG
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1025 GluGlnLeu---------LysLysThrIleSerAspLeuGluGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 AAGCACAAGCACACTGACTACATGAACAAGAGCGACGACTTCACCAACCTGCTGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||
|1038 LysGlu------GluIleIleSerLysSerAspSerSerLysAspGluTyrGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 GAGTTGCAGGCTCGAGAAGATGTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAG
                                                                                                                                                                                                                                              GTTCTGGAGGCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGA
                                                                                                                                                                                                                                                                                                                                                   459 GATGCCATCCTTGCTCAAGAGAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BY, Symington L.S.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCŢION: Required for protein transport from the ER to the Golgi
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: The rodlike tail sequence is highly repetitive, composed of an heptapeptide repeat pattern characteristic of alpha-helical coiled coils. May form filamentous structures in the cell. SIMILARITY: BELONGS TO THE VDP/USO1/YEL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 GAAGATGCAAAAAAAAAGACAAGGCCAATCGGAAGGAG------GAGGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 ATGGCTTCCGGAACTATCAAAAGGCACCTCAAACCATCTGGAGAAAAGTGAGAAAAAAGCT
                                                                                                                                                                                                                                                                                                              SUBCELLUTAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coil.
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CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN FUNCTION.
ASP/GLU.RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stack; Cytoskeleton; Coiled
                                                                               M.K., Herman D.J., Bendel C.M., McClellan M., Tao N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G -> K (IN REF. 2).
E -> K (IN REF. 2).
I -> V (IN REF. 2).
R -> S (IN REF. 2).
R -> S (IN REF. 2).
M, 6CE2B216B9FD4818 CRC64;
                                                                                                        Kendrick K.E.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR0083913, ARM.
InterPro; IPR006955; USO1_D115_C.
InterPro; IPR006955; USO1_D115_C.
InterPro; IPR006955; USO1_D115_C.
InterPro; IPR006956; USO1_D115_C.
IPR006956; USO1_D115_C.
INTERPORT; IPR006956; USO1_D115_C.
INTERPORT; USO1_D15_C.
INTERPORT; USO1_D115_C.
INTERPORT; USO1_D115_C.
INTE
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Cell Biol. 113:245-260(1991)
                                          SEQUENCE OF 782-1790 FROM N.A. Hostetter M.K., Herman D.J., B Kendrick K.E.;
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940 LysMetGlnGlnAsnIleGlnGluLeuGluGluGlnLeuGluGluGluGerAlaAxg 959
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960 GlnLysLeuGlnLeuGluLysValThrThrGluAlaLysLeuLysLysLysLeuGluGluAsp 979
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980 GlnlleIleMetGluAspGlnAsnCysLysLeuAlaLysGluLysLysLeuLeuGluAsp 999
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                                                                                                                                                                                                                                                                                                                                   11 ATP (POTENTIAL).
76 ACTIN-BINDING.
226336 MW; 989876D9681FB19E CRC64;
                                                                                                   Calmodulin-binding; Actin-binding;
                                                                                                                                 IQ.
COILED COIL (POTENTIAL)
                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                   Myosin; ATP-binding; Calmodulin-binding; Actin
Colled coil; Multigene family.
DOMAIN 778 MYOSIN HEAD-LIKE.
DOMAIN 779 808 IQ.
                                                                                                                                                                                                                                                                 US-10-788-793-1 (1-4364) x MYH9_RAT (1-1961)
                Pfam; PF00612; IQ; 1.
Pfam; PF0063; myosin, head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01776; Myosin_Eail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SM0015; IQ; 1.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
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458.50
43.13%
23.49%
5.93%
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1961 AA;
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1454 1281 ------GluLeuAspSerValThrGlyLeuLeuAsnGlnSerAspSerSer 1297 1653 GGGTTGAATAAAAACTTTAAGGTGGAGCAGGGAAAAGTCATGGATGTGACGGAAAAGCTA 1712 1713 ATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGAAAAGGAGTACAGT 1772 1824 AGGTCCTGTGAACTGAGCTGCAGT------GTAGACTTACTAAAGAAG 1865 1866 CGGCTTGATGGCATA------GAGGAGGTAGAAAGGGAAATAAACCGA 1907 1314 -----TAGARTEGAG 1349 1350 AAGCTG---CAGAAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGT 1406 1487 1488 ------GTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGAACTG 1532 1533 GAGAAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATG 1592 1773 CTGACAAAGGAGAGGGATGAGCTGATGGGTAAACTGAGGAGCGAAGAAGAA----- 1823 1050 CACAACCGGCAACTTCGACTCAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAA 1109 1245 ----GGCAAGGATGAAGATCACGAAGAGGT-- 1274 1169 ValSerIleLeuLysLysThrLeudluAspGluAlaLysThrHisGluAlaGlnIleGln 1188 1209 Lys------ArgvalLysAlaThrLeuGluLysAlaLysGlnThrLeuGluAsn 1224 1110 ------GAGACCAATAAAAGCCTTCAGAAGGCAGGAAGAGCTCCAGGAGCTG 1158 AGAGAGAAATTGCCAAAGGGGAATGTGGAAACTTCCAGTCTCATGGCGGAAGTGGAGAGT 1455 CTAACCAAAGACCTGCTGAACGAGCTGGAGGTG--------:::||| |||||::::: 1225 GluArgGlyGluLeuAlaAsnGluValLysAlaLeuLeuGlnGlyLysGlyAspSerGlu |||::: |1265 GluArgValArgThrGluLeuAlaAspLysValSerLysLeuGlnVal------1407 AAGTCGGAATGCACCCAGCTCCATCTGAACCTGGAGAAGGAGAAG-------AAC 1218 CTGCGCAAGCGCGTGCTTGAGATGGAG-----

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resolution.
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SEQUENCE F
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1465 ArgAspArgAlaGluAlaGluAlaArgGluLysGluThrLysAlaLeuSerLeuAla--- 1483
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1484 ---ArgAlaLeuGlu-----GluAlaMetGluGlnLy8AlaGluLeuGluArgLeuAsn 1500
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-----GGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATC 1958
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                                                                                               1445 LysLysPheAspGlnLeuLeuAlaGluGluLysThrIleSerAlaLysTyrAlaGluGlu
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                                                                           1959 AGAGAACTAAACGCTTGAAATCGAGAGTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTG
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01-MAR-1992 (Rel. 21, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aequipecten irradians (Bay scallop).
Bukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
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                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 777-836.
MEDLINE-9417332; PubMed=8127365;
ALE X., Harrison D.H., Schlichting I., Sweet R.M., Kalabokis V.N.,
Szent-Gyorgyi A.G., Cohen C.;
"Structure of the regulatory domain of scallop myosin at 2.8-A
                                                                              Nyitray L., Goodwin E.B., Szent-Gyorgyi A.G.; "Nucleotide sequence of full length cDNA for a scallop striated
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RODLIKE TAIL (S2 AND LWM COILED COIL (POTENTIAL).
ATP (BY SIMILARITY).
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"Structure of the regulatory domain of sci
resolution: implications for regulation."
Structure 4:21-32(1996).
                                                                                                                                      muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990)
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InterPro, IPR004009; Myosin N.
InterPro, IPR002928; Myosin tail.
InterPro, IPR002017; SpectrIn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96419133; PubMed=8805510;
                           TISSUE=Adductor muscle;
MEDLINE=91088319; PubMed=2263488;
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Pfam; PF00063; myosin head; 1.
Pfam; PF02736; Myosin N; 1.
Pfam; PF01576; Myosin tail; 1.
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ProDom; PD000355; myosin_head
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1L2O; 30-OCT-02.
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1WDC; 11-JUL-96.
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1KWO; 20-NOV-02
FROM N.A.
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929 TTACAAATCCAAGGAAGCCGCCAGAAGCTGCTCAAGTTAGAAGTCGACTTCGAACACAA 988   1059ThrdIndluAnnaldIuAspLeuGluArgyalLyst	1096 ileuvalSerGlnLeuGlnArgLysGluLeuGlnAlaArgIleGluGluLeuGl 1116 1109 AGAG	1136	:SerAlaGinileGiuLeuAsniyekyskzgGluhlaGill::: rSerAlaGinileGiuLeuAsniyekyskzgGluhlaGiuLeuLysIleArgAr GGGCAAGGATCACAAGACCAAGGCCAGTGCCGGGAGCTGAAGAAGAAGAG GASDLeuGluGluhlaSerLeuGlnHisGluhlaGinIleSerAlaLeuArgLysLysHi	1304   CCAAGAAGAACACCACAAGGAACTTAGACTAGAAGTGGAGAAGCTGCAGAAGG   1363	rejectiff becaused negatiff the proposed for the construction of t	GTCGGAATGCACCCAGCTCCATCTGAACCTGGAGAAGAAGAACCTAACCAAAGACCT 14 :	1266 IlleAsnGluLeuGinSerGinLysSerArgLeuGinAlaGluAsnSerAspLeuThrAr 1286 1505 AGAACTCGAATGCTCCGAGAGTAGACTG	CCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGATGGATG	GACGAMAGATICALGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1342 uGlnLeuGluGluGluGluGerLysSerAspValGlnArgGlnLeuSerLysAlaAs   1362     1724 CAAGAAGCTTTTAAAACTCAAATGGAAAAGGAGAAAAGGAGTACAGTCTGACAAAGGA 1783	1784 GAGGGATGAGCTGATGGGTAAACTGAGGAGGAAGAAAGGTCCTG 1831 
8 8 8 8	8 & B	& 8 &	2 6 6 8	8 8 8	8 & 8	λ	gg &	6 6 6	3 A &	90 A	λδ Dp
FT HELIX 825 833 FT TURN 834 836 SQUENCE 1938 AA; 222821 MW; ASCCE4127D1A4896 CRC64; Alignment Scores: 9.09e-12 Length: 1938 Score: 457.00 Matches: 234 Per Local Similarity: 43.06\$ Conservative: 213 Best Local Similarity: 22.54\$ Indels: 187 Ouery Match: 1699	-10-788-793-1 (1-4364) x MYS_AEQIR (1-1938) 71 GGGAATGAGATGAGAATCAAGGTGGAGAAAGTTCATCTAACGGCATGTCTCCTGCCC 13	131 131 820	CAAGGCCAATCGGAAGGAGGATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAA uSerllealaArgdinGluGluGluGlu	311 311 871 371	Db   887 nLeuGlnThr	AGAAGACGTCTATGAGAAACCTATCTCAGACAGACAGACTGGAGGAAAAGCA :::	Db 928 pAlaAlaAspLeuGluGlylleLySLySketGluAlaAspAsnAlaAsnLeuLy 948  Qy 602 GCGCACCGTGACGAGAACGAGAAGCACAAGCACACTGACTACATGAACAA 658  Db 948 sLySAspleuGlyAspLeuGluAsnThrLeuGlnDysAlaGluGlnAspLvsAlaGluGAASlaGluGlnAspLvsAlaGluAspLuGAASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLYSASLASLASLASLASLASLASLASLASLASLASLASLASL	GAGCGACGACTTCACCAACCTGCTGGAGCAGGAGCGACGAGGTTGAAAAA	OY 710 GCTCCTTGAACAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAAGGAAAACGCTAAGCGCT 769	Db 1004 rAspSerLeuGlnAlaGluAspLysCysAsnHisLeuAsnLysLeuLysLe 1024  Qy 812 CCTCATGTGGTGGACGAGAGGCAGATGCACTCGAGCAACTGGGCCTGCAGAGTCAGAA 871	102% UCIUCINALALEUABPCIULEUCIUABPABILLEUCIU 872 AGTCCAGGACCTCACTCAGAAGCTGAGGGAGGAAGAAAA

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----TGCAGT----GTAGACTTACTAAAGAAGCGGCTT----GATGG 1876
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                                                    1441 sLysGlnArgAlaPheAspLysThrThrAlaGluTrpGlnAlaLysValAsnSerLeuGl
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nSerGluLeuGluAsnSerGlnLysGluSerArgGlyTyrSerAlaGluLeuTyrArgll
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1521 sGluLeuAspLysAlaArgArgArgLeuGluMetGluLysGluGluLeuGlnAlaAlaLe
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| I638 sThrvalLysArgTyrGlnGlnGlnIleArgGluMetGlnThrSerIleGluGluGluGluGl
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| || | SerSerValGlnGlyGlnLysArgLysLeuGluGlyAspIleAsnAlaMetGlnThrAs
                    rGiuAlaAlaAsnAlaLysCysSerAlaLeuGluLysAlaLysSerArgLeuGlnGlnGl
                                                                                  ---TCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGAACTAAC
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| 11 | UGluGluAlaGluGlyAlaLeuGluGlnGluGluAlaLy8ValMetArgAlaGlnLeuGl
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-1. FURUNIT: Muscle Contraction.

-1. SUBUNIT: Muscle mossin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2).

-1. SUBCELLULAR LOCATION: Thick fillaments of the myofibrils.

-1. TISSUE SPECIFICITY: Smooth muscle, expressed in the umbilical artery, bladder, esophagus and traches.

-1. DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.

-1. DISEASE: A chromosomal rearrangement, known as pericentric inversion Inv(16)(p13;q22), Produces a fusion protein that consists of the 165 N-terminal residues of CBF-beta (PBPB2) with the tail region of MYH1: This rearrangement is associated with acute myeloid leukemia of M4EO subtype.

-1. MISCELLANBOUS: Bach myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
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to chromosomal
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=99425270; PubMed=10493829;

MEDLINE=99425270; PubMed=10493829;

Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,

Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,

Publattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,

Eichler E.E., Harris P.C., Venter J.C.; Adams M.D.;

"Genome duplications and other features in 12 Mb of DNA sequence
human chromosome 16p and 16q.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which co for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kanda
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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[4]
SEQUENCE OF 885-1972 FROM N.A.
MEDLINE=9353189; PubMed=7684189;
Matsucka R., Yoshida M.C., Furutani Y., Imamura S.,
Yanagisawa M., Masaki T., Takao A.;
"Human smooth muscle myosin heavy chain gene mapped
                                                                                                                                                                                                                                                                                                                                           Myosin heavy chain, smooth muscle isoform (SMMHC) MYH11 OR KIAA0866.
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on update)
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01-UUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-WAR-2004 (Rel. 43, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=99156230; PubMed=10048485;
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J. Med. Genet. 46:61-67(1993)
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SEQUENCE OF 1093-1972 FROM N.A.
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1118 GlyHisIleSerAspLeuGlnGluAspLeuAspSerGluArgAlaAlaArgAsnLysAla 1137
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925 HisGluMetGluAlaArgLeuGluGluGluGluAspArgGlyGlnGlnLeuGlnAlaGlu
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1098 ArgLeuAspAspGluIleAlaGInLysAsnAsnAlaLeuLysLysIleArgGluLeuGlu
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366 GluArgGlnGlnLysAlaGluAsnGluLeuLysGluLeuGluGln--------
                                                                                                   CACCGAGATGCCATCCTTGCTCAAGAGAGTCCATAGGAGAAGACGTCTATGAGAAACCT
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945 ArgLysLysMetAlaGlnGlnMetLeuAspLeuGluGluGluLeuGluGluGluGluAla
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-!- SIMILARITY: Contains 1 myosin-like globular head domain.
-!- SIMILARITY: Contains 1 IQ domain.
-!- SIMILARITY: Contains 1 IQ domain.
-!- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWH="http://www.infoblogen.fr/services/chromcancer/Genes/MYH11ID43.html".

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EMBL; AF001548; AAG15212.1; --
EMBL; AF001548; AAG15212.1; --
EMBL; AF001654; ---
EMBL; AG020673; BAA74889.2; ALT INIT.
EMBL; X69292; CAA49154.1; ---
EMBL; EMFO01609; MY081n.head.
EMBL; EMFO01609; MY081n.head.
EMBL; EMFO0193; MY081n.head; 1.
EMBRT; SM00194; MY081n.head; 1.
EMBRT; SM00195; MY081n.head; 1.
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EMBRT; SM00195; MY081n.head; 1.
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CARBOXYL-TERMINAL.

ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (TRI-) (POTENTIAL).

EEK -> NOB (IN REF. 4).

T -> S (IN REF. 4).

KQ -> NE (IN REF. 4).

A -> S (IN REF. 5).

T -> L (IN REF. 5).

T -> L (IN REF. 5).
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785 MYOSIN HEAD-LIKE.
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subfragment (S2).
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---GluLeuAspAspLeuValValAspLeuAspAsnGln---ArgGlnLeuValSerAsn
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CTTCAGCAAGATTTATG 2339
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                                                                                                                                                                                               Isoid=008638-2; Sequence=VSP 003346; DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils. MISCELLANEOUS Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                           2340 GAAGAAGAAACTAAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscle
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-I. FUNCTION: Muscle contraction.

-I. SUBJUIT: Muscle contraction.

-I. SUBJUIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC).

-I. SUBJUIT: Muscle CONTION: Thick filaments of the myofibrils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miano J.M., Ceerjesi P., Ligon K.L., Periasamy M., Olson B.N., "Smooth muscle myosin heavy chain exclusively marks the smooth lineage during mouse embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 myosin-like globular head domain.
SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hasegawa K., Arakawa E., Oda S., Matsuda Y.;
"Molecular cloning and expression of murine smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYHB MOUSE STANDARD; PRT; 1972 AA. 008638; O08639; Q62462; Q64195; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Myyosin heavy chain, smooth muscle isoform (SMMHC) MYH11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biophys. Res. Commun. 232:313-316(1997)
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                                                                                                                                                                                                                                                                                                   GAGCTTTCCAAGCGCTACAGCCGAGCTCTC 2429
                                                                                                                                                                                                                                                                                                                                           ||||
|---AspGluArgLysGlnArgAlaLeu 1614
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MEDLINE-97242182; PubMed-9125171;
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2304 CAAGICGACTATICGGIC-
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954 AAGCTGCTCAAGTTAGAAGTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCAGGAGCAC 1013
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1052 GluLeuGluLysLeuLysArgLysLeuGluGlyAspAlaSerAspPheHisGluGlnIle 1071
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GluGluThrArgSerHisGluAlaGlnValGlnGluMetArgGlnLysHisThrGlnAla 1204
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959 LeuGluGluGluGluAlaAlaArgGlnLysLeuGlnLeuGluLysValThrAlaGluAla 978
                                                                                                                                                                                                                                                                939 GlnGlnLeuGlnAlaGluArgLysLysMetAlaGlnGlnMetLeuAspLeuGluGluGln 958
                                                                                                                                                                                                                                                                                                                                                                        615 GAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAACAAGAGCGACGACTTCACC
                                                                                                                                                                                                             675 AACCTGCTGGAGCAGGAGCGAGAGGG--------TTGAAAAAGCTC
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|1085 LeuAlaLysLysGluGluGluLeuGlnAlaAlaLeuAlaArgLeuAspGluGluIleAla
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                          435 AAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGAGAAGTCCATAGGAGAA
                                                                                 495 GACGICIAIGAGAAACCIAICICAGAGCIGGACAGACIGGAGGAAAAGCAGAAGGAGACG
                                                                                                                                      555 TACCGCCGCATGCTAGAGCAGCTGCTGCTGAGAAGTGTCACAGGCGCACCGTGTAC
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                                             867 ArgGlnGlnLysAlaGluThrGluLeuLysGluLeuGlu-
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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10.
COLLED COIL (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL).
RGNEASFVERRAGERRUTENTOGSBEEMDARDSDFNGTKA.
SE -> GPPOPENSQ (In isoform 2).
FTIGA-SYP 003346.
N -> D (IN REP. 3).
A -> V (IN REP. 2).
26 MW; Al399B3F5B11F15A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            827 LeuLysLeuArgAsnTrpGlnTrpTrpArgLeuPheThrLysValLysProLeuLeuGln 846
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807 ThrLysArgGlnGlnGlnLeuThrAlaMetLysVallleGlnArgAsnCysAlaAlaTyr
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AsplysValHislysLeuGln-------AsnGluValGluSerVal 1292
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|1242 ValLeuGlyGlnAlaLysGlnGluValGluHisLysLysLysLysLeuGluValGlnLeu 1261
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ATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAG 1424
                                                         CTCCATCTGAACCTGGAGAAGAAGAACCTAACCAAAGACCTGCTGAACGAGCTGGAG 1484
                                                                                     SerLysGlnThrLeuGluLysGlu-----AsnAlaAspLeuAlaGlyGluLeuArg 1241
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|AspGluGluMetGluAlaLysGlnAsnLeuGluArgHisValSerThrLeuAsnIleGln 1372
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LysPheAspGlnLeuLeuAlaGluGluLysAsnIleSerSerLysTyrAlaAspGluArg 1471
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1492 LeuGluGluAlaLeuGluAlaLysGluGluLeuGluArgThrAsnLysMetLeuLysAla 1511
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1532 LysSerLysArgAlaLeuGluThrGlnMetGluGluMetLysThrGlnLeuGluGluSer 1551
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1293 ThrGlyMetLeuAsnGluAlaGluAlaGlyLysAlaIleLysLeuAlaLysAspValAlaSer
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                                                                                                                  -----GTCAAGAGTCGAGTTAAAGAACTCGAA----
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1592 ArgGlnLeuGlnArgGlnLeuHisGluTyrGluThrGluLeuGlu---AspGluArgLys 1610
                                                                                                                                                          2358 AAGAACATGGGGAGGGGGGGTCCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGCTAC 2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                   1552 GluAspAspValGlnAlaThrGluAspAlaLysLeuArgLeuGluValAsnMetGlnAla 1571
-----CTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTC 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capping.

Subunt: Myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2).

DOMAIN: The rodilke tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coils.

SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                             ----CTTCAGCAAGATTTATGGAAGAAGAACTAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular myosin.";
Proc. Natl. Acad. Sci. U.S.A. 86:7726-7730(1989).
-!- FUNCTION: Cellular myosin appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and
                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, nonmuscle (Cellular myosin heavy chain) (NWMHC)
MYH9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Intestinal epithelium;
MEDLINE=90046668; PubMed=2813355;
Shohet R.V., Conti M.A., Kawamoto S., Preston Y.A., Brill D.A., Adelstein R.S.;
                                                                                                                                                                                                                                                                                                                                                            PRT; 1959 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P10587, 1BR2.
InterPro; IPR0010048; IQ region.
InterPro; IPR001609; myosin.head.
InterPro; IPR004009; Myosin.N.
InterPro; IPR002928; Myosin.Ltll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00063; myosin head; 1.
Pfam; PF02736; Myosin N; 1.
Pfam; PF01576; Myosin tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin head
SMART; SM00015; 1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M26510; AAA48974.1; -. PIR; A33977; A33977.
                                                                                                                                                                                                                                       2418 AGCCGAGCTCTC 2429
                                                                                                                                                                                                                                                                            1611 GlnArgAlaLeu 1614
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                            CHICK
2271
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HUMAN
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1483 ArgAlaLeuGlu-----GluAlaIleGluGlnLysAlaGluLeuGluArgValAsnLys 1500
                                                                                                                                                                                                                                                                                2204
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|ValAsnGlnGlnAlaMetLysAlaGlnPheAspArgAspLeuLeuGlyArgAspGluGln 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                2402
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                                                                                                                                                                                              GATAAGGCAAACTICCTCTCCCAGCAGCTCGAGGAAATCAAACACCCAAATGGCCAAGCAC 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1679 GlualaGluMetIleGlnLeuGlnGluGluLeualaalaalaGluargAlaLysArgGln 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ala-----GlnGlnGluArgAsp 1704
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|||| ::: ||||||
|386 AlaLysLysLysLeuGlnLysAspLeuGluSerLeuThrGlnArgTyrGluGluLysIle
                                                                      1959 AGAGAACTAAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCCAGCAG---TTGGAGGTG
                                                                                      1406 AlaAlaTyrAsp---LysLeuGluLysThrLysThrArgLeuGlnGluLeuAspAsp
                                                                                                                ------TTGATGAAGACCGAGGAC
                                                                                                                               1425 IleAlaValAspLeuAspHisGlnArgGlnThrValSerAsnLeuGluLysLysGlnLys
                                                                                                                                                                     1501 GlnPheArgThrGluMetGluAspLeuMetSerSerLysAspAspValGlyLysSerVal
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---AspGluArgLysGlnArgSerIleAlaValAlaAlaArgLysLysLeuGluLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2463 GTGCCTGTGGCCTCCACTGGGGTGCAGACCGAGGGGGTGTGCGGGGATGCTGCGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuLysAspLeuGluSerHisIleAspThrAlaAsnLysAsnArgAspGluAlaIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2733 CCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGGAGCTGGTCCTAGCACCAAAGCAGGGC
                              ATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATC
                                                                                                                                                       --GAGCAGAAGTTCAGAACCGAGCAG
                                                                                                                                                                                                                  1465 AspArgAlaGluAlaGluAlaArgGluLysGluThrLysAlaLeuSerLeuAla----
                                                                                                                                                                                                                                       AAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACAC-----
                                                                                                                                                                                                                                                                                                                        CTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                AAGATCCACGAGCTGATGAACAAG------GAAGACCAGCTGTCTCAGCTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                        2343 GAAGAAACTAAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2403 CTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGAC
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1705 GluLeuAlaAspGluIleAlaAsnSerSerGlyLysGlyAlaLeuAlaMetGluGluLys 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE CYTOSKELETON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOId=P30622-2; Sequence=VSP_000765;
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H., Asselbergs F.A.M.
Wiesendanger W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-Peripheral blood monocytes;

TISSUE-Peripheral blood monocytes;

BELINRE-2228675; Pubmed-1600942;

Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M. Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W., de Wolf-Peeters C., Shipman R.;

"Restin: a novel intermediate filament-associated protein highly expressed in the Reed-Sternberg cells of Hodgkin's disease.";
                                                                                                                                                                                                                                                                                                                                                                                                         (CLIP-170) (Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=92405160; PubMed=1356075;
Pierre P., Scheel J., Rickard J.E., Kreis T.E.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Last sequence update)
8=FEB-2003 (Rel. 41, Last annoctation update)
Restin (Cytoplasmic linker protein-170 alpha-2) (CL sternberg intermediate filament associated protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
Name=Long;
                                                                                                                                                                                                                                                   PRT; 1427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 2 CAP-Gly domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P30622-1; Sequence=Displayed;
                                                          2793 CAGCCCCTACACATCCGTGTG 2813
                                                                                                 SMART; SM00343; ZnF C2HC; 1.
PROSITE; PS00845; CAP_GLY_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X64838; CAA46050.1; -. EMBL; M97501; AAA35693.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HODGKIN'S DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001878; Znf
Pfam; PF01302; CAP GLY;
SMART; SM00343; ZnF C2HC
                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (Human)
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                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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PROSITE; PS50245; CAP GLY 2; 2.	<b>q</b> 0	708 LysAlaGluAspGlnHisLeuValGluMetGluAspThrLeuAsnLysLeuGlnGlu 726
Cycoskeleton; Microtubule; DOMAIN 78 120	ò	831 AGGCAGATGCACATCGAGCAACTGGGCCTGCAGAGTCAG 869
DOMAIN 232 274	qa	727 AlaGluIleLysValLysGluLeuGluValLeuGlnAlaLysCysAsnGluGlnThrLys 746
DOMAIN 350 1342 DOMAIN 1408 1421	ζŏ	870 AAAGTCCAGGACCTCACTCAGAAGCTGAGGGAAGAAAAAAAA
VARSPLIC 457 491	qa	747 ValileAspAsnPheThrSerGlnLeuLysAlaThrGluGluLysLeuLeuAspLeuAsp 766
FT CONFLICT 1069 1069 D -> E (IN REF. 2). SQ SEQUENCE 1427 AA; 160989 MW; 0A4F166DD94254E8 CRC64;	۶ ۶	921 GCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTC 980
Alignment Scores: 2.29e-11 Length: 1427 Score: 447.00 Matches: 196 Percent Similarity: 43.62% Conservative: 187	G & G	GAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAGTGTGTGT
: 22.324 mismacches: 5.78\$ Indels: 1 Gaps:	Qy Db	1041 CAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTTGGCTTATCGCAA 1091
US-10-788-793-1 (1-4364) x REST_HUMAN (1-1427)	è	
OY 174 GAAGATGCAAAAAAGAACAAGGCCAATCGGAAGGAGGATGTCATGGCTTCCGGAACT 233	e 40	AsnLeuSerGluValSerGlnValLysGluThrLeuGluLysGluLeuGln
234ATCAAAAGGCACTCAAACCATCTGGAGAAAAGTGAG 26	À 1	1152 GAGCTGAGAGAAATTGCCAAAGGG
Db 496 SerGluLysSerArglleMetGluLeuGluLysAspLeuAlaLeuArgValGluVal 515		
OY 270 AAAAGACTAAGAAGTCTGTGAGTTATCCAAGGAGGACCTCATCCAGCTCCTG 323		:::     ::::::::::::::::::::::::::
324 AGTATCATGAAAGGGAAGGGAGGCAAAAAAAAAAATGATCATCCAAATGCTGAAGAAGAA 38	33 624	1209 GTGGAGAGTCTGGGCAGAGGGGGTGCTTGAGATGGAGGGCAAGGATGAAGATCACGAAG 1268 1.
Db 536 SerLeuLeuGlnGlulleSerSerLeuGlnGluLysLeuGluValThrArgThrAsp 554		ACCGAGGCCCAGTGCCGGGAGCTGAAGAAGCTCCAAGAGAAGAAGTCCAAGAGAA
Qy         384 AAAACCAAGCCCGAGGTTCTGGAGGCACACTATGGATCTGCAGAACCT 431           Dh         555 Hischbard		 ArgGluGluGlnLeuIleiysAlaLysGluLysLeuGluAsnAsp1leAlaGluIleMet
432 GAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGAGAAGTCCATAGGA	03	1313 1313
		LysMetSerGlyAspAsnSerSerGlnLeuThrLysMetAsnAspGluLeuArgLeuLys
Qy         492 GAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACGGAC	1 0y	1314 GAACACCAAGGAACTTYGAACTAGAAATGGAAGAACTGCAGAAGAGGATGTCTCTGAG 13/3
552 ACGIACCGCCGCAIGCIAGAGCAGCTGCTGCTGGCTGAGAAGTGTCACAGGGGCACCGTG	1 Qy	1374 CTGGAGAAGCTGGAGGGATCAGCCGGAGTAAGTCGGAATGCACC 1421
Db 608 ValileAlaLeuTrpLysSerLysLeuGluThrAlaIleAlaSerHisGlnGlnAlaMet 627		CAGCTCCATCTGAACCTGGAGAAGAAGAAGAACTAACCAAAGACCTGCTGAAAGAGTG
Oy 612 TACGAGATGGAGAAGGACAAGG		:::
639CACACTACACTACACAGAGGGACGACTTCACC	\$ &	1482 GAGGTGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAG 1535
ıleglu		PAGGCCGAGTTTAAGCCTTCAAAGATGACCTTACAAAGCCAGAAGTCCTTCACTGATGATGATG
OY 675 AACCTGCTGGAGCAGAGAGAGTTGAAAAAAGCTCCTTGAACAAGAAAAA 728  DD 668 ASHGILGIDASDSSECIUMYAAJAAJAHISAAJALVSGIUMEGIUAJALEUAXCAJAAYS 687	<del></del>	
729 GCTTACCAAGCCGCAAAGAAAAGGAAAACGCTAAGCGGCTCAAC		GTGGATGAGAAAAATATGATGGAQAAAATAAAGCAAGAAGAGAGGAAAGTGGATGGG
:::		GINASNIEWGINLYSTREHEUEURASPINIGIUASPLYSHEUL 
OY 774 AAACTICGAGAIGAGCTIGIGAAGCICAAAGTCCTICGCCCTCAIGITGGIGGACGAG 830	, a	uArgLys

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1829
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CTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGGAAAAGGAGTAC 1769
                                                                                                                                                                                                                           -----LysSerLysGluLeuLeuThrValGluAsn 1137
                                                                                                                                                                                                                                                             1997
                                                                                                                                                                                                                                                                                        GlnLysMetGluGluPheArgLysGluIleGluThrLeuLysGlnAlaAlaAlaGlnLys 1157
                                                                                                                                                                                                                                                                                                                                                                                         2058 TTGGAGCAGAAGTTCAGAACCGAGCAG------GATAAGGCAAACTTCCTCTCCCAG 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fierz M.J., Rogers G.E.,
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Intermediate filament-associated protein that associates
in regular arrays with keratin intermediate filaments (KIF) of the
inner root sheath cells of the hair follicle and the granular
                                                                                                                                                                                                                                                                                                                                                                                                               ::: |||::: |||| SerArgAspGluValThrSerHisGlnLysLeuGluGluGluArgSerValLeuAsnAsn
                                                                             ||||||||| serdlnGlnLeuSerAlaLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnLeuGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnAlaAspLysAlaLysAlaAlaGlnThrAlaGluAspAlaMetGlnIleMetGlu---
                                                              AGTCTGACAAAGGAGGATGAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAGGTCC
                                                                                                                           TGTGAACTGAGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGAGGTA
                                                                                                                                                                                           GAAAGGGAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGAC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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01-OCT-1994 (Rel. 30, Last sequence update)
101-OCT-2003 (Rel. 42, Last annotation update)
Trichohyalin.
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SUBUNIT: Homodimer (Probable).
SUBUNIT: Homodimer (Probable).
SUBUNIT: PECIFICITY: Found in the hard keratinizing tissues such as the inner root sheath (IRS) of hair follicles and medulla, and in the filliform papillae of dorsal tongue epithelium (Probable).
DEVELOPMENTAL STAGE: Expressed during late differentiation of the epidermis.

DOMAIN: Consists of nine domains. Domain 1 contains two EF-hand calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domain 6 is bomains 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among 524 TrpGlnLeuGlnGluAlaGlnArgArgArgHisThrLeuTyrAlaLysProGlyGln CGGGCATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGATGGTGGTAAGGGCCCCTC probably converted to citrullines by peptidylarginine deimidase. SIMILARITY: In the N-terminal section; belongs to the S-100 SIMILARITY: Contains 2 EF-hand calcium-binding domains. transglutaminase. Some 200 arginines TGGGTTCTTCAAGGGATAAACCAGCGGCGAAAGAACACA----:::|||
544 GlnGluGlnLeuArgGluGluGluGluLeuGlnArgGluLys---1407 227 182 343 228 40 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-1407)US-10-788-793-1 (1-4364) x TRHY\_RABIT 2.64e-11 445.50 41.73% 23.16% 5.76% different species. PTM: Substrate of t Similarity: Percent Similarity: ß 113 Query Match: DB: Best Local + ---+ -%FFFF% 요 g à ò ò

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ACTTCCTCTCCAGCAGCT 2113 ATGGAGAAATAAAGCAAGA 1636 |||::: ::||||| 3luGluGlnPheArgGlnGl 1047 AGAGGGATGAGCTGATGGG 1801 ||||||||| ||uArgAspArg----- 1098 GCAGTGTAGACTTACTAAA 1861 ACCGAGGTAGGTCGTGCAA 1921 luargalaargiysieuar 1125 CCTGCCCGGAAGACAATAA 1954 rgGlnGluArgAspArgLy 1145 AGGACGAATATGACCAGTT · 2059 || ||| ||| |luArgGluGluGluArgLe 1185 AGAAAGGGGAGGCCGTGAG 2173 AGAACCTAACCAAAGAC-- 1466 :: rgLysPheArgGluGluGl 1008 AAGAACTCGAATGCTCCGA 1522 ------dl 1016 ATGACCTTACAAAGCTGAA 1576 ::::: luGluGluArgGlnLeuAr 1036 AGCAGGGAAAAGTCATGGA 1696 ||::: |uGluGlnIleArgGlnGl 1061 AGCGCGTGCTTGAGATGGA 1243 CCCAG-----TGCCGGGA 1288 AACTTAGACTAGAAGTGGA 1348 AAGCGTTCAGCCGGAGTAA 1408 AACTCAAATCTGAA---- 1751 || ::: ||| ysPheArgGluGluGluGl 1081 :: ||| .rgLysLeuArgGluGlu-- 915 euArgArgGlnGluArgGl 933 ||| |uGlnGluLeuArgArgGl 953 ll luArgGluGluGluArgLe 973 :: |||| | InteufeuArgArgGluGl 993

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Proc. Natl. Acad. Sci. U.S.A. 88:10676-10680(1991).

-!- FUNCTION: Muscle contraction.
-!- FUNCTION: Muscle contraction.
-!- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MLC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC).
-!- SUBCELULAR LOCATION: Thick filaments of the myofibrils.
-!- DOWAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
-!- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light... meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
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gArgGlnLeuArgGluArgGlnPheArgGluAspGlnSerArgArgGlnValLeuGlu 1378
                                                                     2396 GCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGGGAACGGCCGAAGGAT
                                                                                                                                                -----GCTAAAAGTCGTGATTTACAGGCCGAGGTGCA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, smooth muscle isoform (SMMHC)
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906 AlaGluGluMetArgValArgLeuAlaAlaLy8Ly8GlnGluCeuGluGluIleLeuHis 925
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R Pfam; PF00612; 10; 1.

R Pfam; PF00613; Myosin_head; 1.

R Pfam; PF02736; Myosin_N; 1.

R Pfam; PF01776; Myosin_Lail; 1.

R RINTS; PR00193; MyOSINHEAVY.

DR SMART; SM00195; MyOSINHEAVY.

DR SMART; SM00192; MYSC; 1.

DR SWART; SM00196; 10; 1.

DR Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Myosin; Multigene family.
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ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL)
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COILED COIL (POTENTIAL).
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InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR00228; Myosin_N.
InterPro; IPR002017; Spectin.
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Best Local Similarity:
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Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.,
"Complete sequence of the Drosophila nonmuscle myosin heavy-chain
transcript: conserved sequences in the myosin tail and differential
splicing in the 5' untranslated sequence.";
Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).
-!- FUNCTION: Nonmuscle myosin appears to be responsible for
cellularization. Required for morphogenesis and cytokinesis.
                                         SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
                                                                                     MEDLINE=90349606; PubMed=2117279;
  NCBI_TaxID=7227;
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-----ATCGAGAGACTG 1988
                                     1683 LysSerLeuGluAlaAspLeuMetGlnLeuGlnGluAspLeuAlaAlaAlaGluArgAla 1702
                                                                                                                                                                                                                                                                                   1803 GluMetGluGlyAlaValLysSerLysPheLysSerThrIleAlaAlaLeuGluAlaLys 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||||||:::
|1843 AlaLeuLysGlnArgAspLysLysLeuLysGluMetLeuLeuGlnValGluAspGluArg 1862
                                                                                                                                                                                                                                                      CAGAAGTTCAGAACCGAGCAG-------CATAAGGCAAACTTCCTC 2102
                                                                                                                                                                                                                                                                                                                                                                                      1782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1863 LysMetAlaGluGlnTyrLysGluGlnAlaGluLysGlyAsnAlaLysValLysGlnLeu 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2277 -------AACAAGGAAGACCCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTC 2321
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LyshrgGlnLeuGluGluAlaGluGluGluSerGlnArgIleAsnAlaAsnArgArgLys 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCAGCAAAGATTTATGGAAGAAGAACTAAGAACAAGAACATGGGGAGGGGGGGCTCCTC 2381
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                                                                                                                                                                                                                                                                                                                                                              :::|||:::
1703 ArgLysGlnAlaAspLeuGluLysGluGluLeuAlaGluLeuAlaSerSerLeuSer
                                                                                                                                                                                                             1723 GlyArgAsnAlaLeuGlnAspGluLysArgArgLeuGluAlaArgIleAlaGinLeuGlu
                                                                                                                                                                     ----GGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAG
                                                                                                                                                                                                                                                                                                                                          TCCCAGCAGCTCGAGGAAATCAACACCCAAATGGCCAAGCACAAAGCC---ATAGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                              2160 GGGGAGGCCGTGAGCCAGGAAGCCGAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CTGGAG-----GAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                 AAGAAACGG-----CTCCAGCAGTTGGAGGTGGTGGAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1950 AsnAlaAspGlySerGluGluGluValAspAla 1960
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(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CTGCGACACAGGTTTCGG---
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1965 CTAACGCTTGAA-----
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50 kDa/20 kDa JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING.
LIGHT MEROWYCOSIN (LAW).
ALPHA-HELICAL TALLPIECE (LAW).
GLOBULAR TAILPIECE.
                                                                                                         IBGIG=099323-2; Sequence=VSP 003342; SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P10587; 1BR2.
FlyBage; FBGN005534; zip.
G) GO:0005856; C:cytoskeleton; NAS.
GO; GO:0005866; C:non-muscle myosin; NAS.
GO; GO:0046663; P:leading edge cell differentiation; IMP.
GO; GO:0006536; P:medcle contraction; IMP.
GO; GO:0045214; P:marcomere organization; IMP.
GO; GO:007395; P:spreading of leading edge cells; IMP.
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lin-binding.
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Event=Alternative splicing; Named isoforms=2;
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Matches:
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InterPro; IPR001609; myosin head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
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Pfam, PF00063; myosin_head, 1.
Pfam, PF02736; Myosin_N; 1.
Pfam, PF01576; Myosin_tail; 1.
PRINTS, PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M35012; AAA28713.1; -.
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SMART; SM00242; MYSC;
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ATP-binding; Calmodul
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1120   IGINVALNEPGLUWECGINALGENTIABAPKEGLUGIUGIUGIULEUTRICITITALE   1140   1161   11	1982 GAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGAGGGGGAGCTTGATGATGAAGACCGA 2041
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### ### ##############################	1100 rLyBArgLyBIleGluThrGluValAlaAspLeuLyBGluGlnLeuAsnGluArgArgVa 1120 1007 GGAGCACGAAGAGATGAACGCCAAATTGGCGAATCAAGAATCTCACAACCGGCAACTTCG 1066 ::: :::              :::        :::

3002	DD 1794 rAsnSerGluValLeuLeu 3021 - actactatttccacacac	1814		Db 1834 uGluArgGlnAsnLysGlu	3080	Db 1854 rLysValLysAlaThrile Ov 3140 CTCTCCTGAATCTCAGGAA	1874	Qy 3200 ACAAACTGTTCCAGCCCCC	1886	Db 1901 nIleGluAspGluAspGluArgArg	Qy 3290 TCAGTTTAAG	Db 1921 rArglleLysLeuLeuLys	3341	DD 1941 BIRKGINLYBAEGLYBIYE	1961	3446	1981 rSerSerArgLeuTh	Db 2001 pAspSerSerValGlnAsp	RESULT 14 REST_CHICK	ID REST CHICK STANDARD; AC 042184; 042228; 057563; 05756	DT 15-JUL-1998 (Rel. 36, Last a DT 10-OCT-2003 (Rel. 36, Last a DT 2003)	DE REBLIN (CYCODIABMIC LINKEL DO GN RSN.	sailus yailus Sukaryota; Met Archosauria; A	OC Gallus. OX NCBL_TaxID=9031;	RX NEDLINE=98137792; PubMed=946	RA Griparic L., Volosky J.M., K. RT "Cloning and expression of cl	<pre>RL Gene 206:195-208(1998). RN [2]</pre>	RP SEQUENCE OF 17-1139 FROM N.A R TISSUE-PECARALIS muscle; RX MEDLINE-99002898; Pubmed=978 RA Griparic L., Keller T.C. III
2042 GGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACCGAGGCAGGATAAGGCAAACTTC 2099	  1459 nAspArgLeuAspLysSerLysLysLysIleGlnSerGluLeuGluAspAlaThrIleGl 1479	2100	uLeuGluAlaGlnArgThrLysValLeuGluLeuGluLysLysGlnLysAsnPheAspLy	2129 CCAMPIGGCCCARGCACCAINGAGAAGGGGGAGCCGGGAAGCCGAAGT 2188   2199   SIleLeubladiuGluLysblall	GCGACACAGGTITCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCA		GGCTCTCAAGGAGAGAGTCCACGAGCTGATGAACAAGGAA	155/ perualakneaspuysileeluaspueudilaasnuysakguysinineudinasnelue 155/ 2286 -GACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTC	:::	CTTCAGCAAAGATTATGGAAGAAACTAAGAACAAGAAGAGGGGGGGG	15// abjekrigktabeugiuserginbeuktagiubeubjeklagiuheubseruginkeuGi 1596 2372 gaaggiothoatphgalcaacgaghtagistarintoaaggartagagintagag 241	asspanpleuGlnLeuThrGluaspalaLysLeu	2432 GCCGAGTGGGAACGGCCGAAGGATGGACGTGCCTGTGGCCTCCACTGGGGTGCAGAC 2491	1608ArgLeuGluValAsnMetGlnAlaLeuArgSerGlnPheGluAr 1622	2492 CGAGGGGTGTGCGGGATGCTGCGGAGGAGAGACCCCGGGTGTGTTCGTTC	CTTCCAGGAGGAAAATCACATCATGAGTAATCTTCGACAGGTAGGCCT		2600 GAAGAAACCCATGGAACGGTCCTCGGACAGGTATCCCCCAGCAGCGAATGAGCT 2659	CACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAAGAGAAAA	:::::: 	CGGTCCTTCCACCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACCC	1/00 ABPATALEUNIGABPATAGLIUALALABARTAANABALUGIULEUGIINALAEUSET 1/19 2262 GGGGGAGGAGGARGARGARGARGARGARGARGARGARGAR		2822 TCATGAGAACAGCACTGCACCCTGGAGATCACAAGCCCCACATCTGAAGAGTTTTCTC 2881	1739 preualaSerSerGluargalaargargalaalaGluThrGluargaspGluLeualaGl 1759	CACCGTCATTCCTAGGCAACCAGAAACCAAGAATAACCATTATTCCATC	uGlulleAlaAsnAsnAlaAsnLysGlySerLeuMetIleAspGl	2942 ACCCAATGTCGCAAAAGCCCAAAAGTGCAGATCCTACTCTCGGCCCAGAACGAGC 3001 1774 uLy8ArgArgLeuGluAlaArg1leAlaThrLeuGluGluGluGluGluGluGluGluGluGluGluGluGl
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GCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCAGTTAT 3340
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uAspArgAlaAlaAlaArgGlnLeuGlnIleGluGlnLeuTh 1814
                                              GAAGAGC------CCGGAAGGTGGAAGGAGCGCCTT 3067
                                                                        |||||||
|UysSerAsnSerGlnLysAsnGluAsnGlyArgAlaLeuLe 1834
                                                                                                                                    ------GCCGACAGGCC 3079
                                                                                                                                                                       uLeuLysAlaLysLeuAlaGluIleGluThrAlaGlnArgTh 1854
                                                                                                                                                                                                                           CATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGT 3139
                                                                                                                                                                                                                                                           AGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCGGAAAA 3199
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----ArgLysMetAspLysLysIleLysGluLeuThrMetAs 1901
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gHisValAspGlnHisLysGluGlnMetAspLysLeuAsnSe 1921
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|ArgAsnLeuAspGluThrGluGluGluLeuGlnLysGluLy 1941
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yThrProSerSerLysArgAlaGlyGlyGlyGlySerAs 2001
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nae; Galliformes; Phasianidae; Phasianinae;
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Keller T.C. III;
chicken CLIP-170 and restin isoforms.";
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spGluSerLeuAspGlyGluAspSerAlaAsn 2017
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annotation update)
protein-170) (CLIP-170).
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T.C. III;
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960 CTCAAGTTAGAAGTGGACTTCGAACACACAGGCCTCG-----AGGTTTTCCCAGGAGCAC 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1191 TCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGCGTGCTTGAGATGGAGGGCAAG 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1251 GATGAAGAGATCACGAAGACCGAGGCCCAGTGCCGGGAGCTGAAGAAG------AAG 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||| :::|||:::|||::: ||| GluSerIleThrLysGlyAspLeuGluThrGlnThrLysLeuGluHisAlaArgIleLys 468
                                          ------ATGCTGAGGACAGAAAACCAAGCCCGAGGTTCTGGAGGCACACTAT 416
                                                                                                                                                                                                                                                                                                       621 GAGAACGAGAAGCACAAGCACACTGACTACATGAACAAGAGCGACGACTTCACCAACCTG 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            732 ValLysGluLeuAspValLeuGlnAlaLysCysAsnGluGlnThrLysLeuIleGlySer 751
                                                                                                                                                                                                                                                                                                                                                                       GGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAA
                                                                                                                    ---GluLeuGluAspThrArgValAlaThrValSerGluLysSerArgileMetGluLeu
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506 GluArgAspLeuAlaLeuArgVal-----LysGluValAlaGluLeuArgGlyArgLeu
                                                                                                                                                                                                  534 GAGGAAAAGCAGAAAG------GAGACGTACCGC
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524 GluSerSerLysHisIleAspAspValAspThrSerLeuSerLeuLeuGlnGluIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                     587 ArgMetGlyLysGluAsnGluSerLeuLysThrLysLeuAspHisAlaAsnLysGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                               783 GATGAGCTTGTGAAGCTC---AAGTCCTTCGCCCTCATGTTGGTGGACAAGGCAGATG
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                                                                                                                                                                                                                                                                             544 SerLeuGlnGluLysMetAlaAlaAlaGlyLysGluHisGlnArg------GluMet
                                                                                                                                                                                                                                                                                                                                                                                                             741 CGCAAAGAAAAGGAAAACGCTAAG-------CGGCTCAACAACTTCGA
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                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAGTGAGAAAAAGACTAAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTC 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coiled coil; Repeat; Alternative splicing. CAP-GLY 1. SER-RICH. CAP-GLY 2. SER-RICH.
   "Identification and expression of two novel CLIP-170/Restin isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTIGaVEP 000761.
TOTKERARIKEBOSLIEERKKADKLQRELEDTR ->
RQISEDPEN (in isoform 3).
/FTIGaVEP 000762.
S -> GGSSKVS (in isoform 3).
/FTIGaVEP 000763.
T -> RKAQISEDPENT (in isoform 4).
/FTIGaVEP 000764.
K -> R ITM RRF. 2; AAC03549).
E -> V (IN RRF. 2; AAC03548).
          CTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGAAGATGTCATCCAC-
                                                                                                                                                                                                VSP_000763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL)
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Missing (in isoform 2).
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                   Name=3; Synonyms=CLIP-170(11);
IsoId=042184-5; Sequence=vSP_000762,
IsoId=042184-5; Sequence=vSP_000762,
Name=4; Synonyms=CLIP-170(11+35);
IsoId=042184-4; Sequence=vSP_000764;
SIMILARITY: Contains 2 CAP-Gly_domains.
                                                                                                                               Name=1;
IsoId=O42184-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF014012; AAC60344.1; --
EMBL, AF0207045, AAC60345.1; --
EMBL, AF045650; AAC03545.1; --
EMBL, AF045651; AAC03548.1; --
EMBL, AF045651; AAC03548.1; --
INTERFPO: IPR0010938; CAP-Cdly.
INTERFPO: IPR0010878; ZAF-CGly.
PFam; PF01302; CAP_GLY; Z.
PROSTIE; S000345; CAP_GLY; 1, 2.
PROSTIE; PS50245; CAP_GLY, 1, 2.
CYCOKFOLEON; Microtubule; Coiled
DOMAIN
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752 LeuThrGlnGlnIleArgAlaSerGluGluLysLeuLeuAspLeuAlaAlaLeuGlnLys	1362 AGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGAGTAAG	1410 TCGGAATGCACCCAGCTCCATCTGAACCTGGAGAAGGAGAAGCTAACCAAAGACCTG :::	1470 CTGAACGAGCTGGAGGTGGTCAAGAGTTGAAAGAACTCGAATGCTCCGAGAGTAGA	ភូ ::	826 ValAsnGinValLysAspSerLeuGluLysGluLeuGlnLeuLeuLysGluLysPheThr 1590 angregenganganganaaaansmangangganaaansmanganganaaan	1950 AICCIGGICGAIGAGAGAAAAAAAAAAAAAAAAAAAAAGAGAGAG	1650 GATGGGTTGAATAAAACTTTAAGGTGGAGCAGGGAAAAGTCATGGATGTGACGGAAAAG	1710 CTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGGAAAAGGAG		 GlnGlnLeuThrGluAlaLy8V	1815 GAAGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTAAGAAGCGGCTTGAT	921 SerGlyAspSerSerAlaGlnLeuMetLysMetAsnAspGluLeuArgLeuLysGluArg	1875 GGCATAGAGGAGGTAGAAAGGGAAATAAACCGAGGTAGGT	1920 AAGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGAACTAACGCTTGAAATC	961 LysAsnValGluGlnThrAlaGlnLysAlaGluGlnSerGlnGlnGluThrLeuLysThr	1980GAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGACTTGATG	2034 AAGACCGACGACGATATGACCAGTTGGAGCAGAAGTTCAGAACCGAG	1001 ThrSerGlnAsnGlnTyrLysAspLeuGlnAlaLysTyrGluLysGluThrSerGluMet	2081	1021 IleThrLysHisAspAlaAspIleLysGlyPheLysGlnAsnLeuLeuAspAlaGluGlu	2082CAGGATAAGGCAAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAA		117 CACCAATUGECCAAGCCGAAGCCATGAGGAGAAGGGGGGGGGGGGGGG	2187 CTGCGACACAGGTTTCGGCTGGAGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAG	1081AlalleHisGluLysAspAlalleHisGlu	2247 GCTCTCAAGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAA 1092 GluLysIleGluThrLeuAlaSerLeuGluAsnSerArgGlnThrAsnGluLysLeuGlu
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-----GluileThr 1248 2415 TACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGACGTGCCTGTGGCC 2474 |||||||::: :::
1148 GluPheGluAlaLeuLysLeuAlaAlaAlaGlnLysSerGlnGlnLeuAlaAlaLeuGln 1167 -----CTTCGACAGGTAGGCCTGAAGAACCCATG-----GAACGGTCCTCGGTCCTC 2630 2631 GACAGGIATCCCCCAGCAGCAGCAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATG 2690 2691 AGAAAAAGAGAAAACGGTCCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGT 2750 2751 GCAGGGCACCCCGGGGAGCTGGTCCTAGCACCAAAGCAGGGCCAGCCCTACACATCCGT 2810 2811 GIGACACCAGATCATGAGAACAGCACTGCCACCTGGAGATCACAAGCCCCACATCTGAA 2870 2871 GAGTITITICICIAGIACCACCGICATICCTACCITAGGCAACCAGAAACCAAGAAIAACC 2930 2991 CCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGAGAGAAGAGCCCGGAA 3050 :::::: ||||||| 1286 LysAlaLysSerGluGlnProLeuThrValThr-------SerProSer 1299 3051 GGTGGAAGGAGCGCC----TTTGCCGACAGGCCTGCATCC------3086 . ||| :::||| 1300 GlyAspIleAlaAlaAsnLeuLeuGlnAspGluSerAlaGluAspLysGlnGluIle 1319 1320 AspPheLeuAsnSerValIleValAspLeuGlnArgArgAsnGluGluLeuAsnLeuLys 1339 3210 CCAGCCCCCGTGCGGA------3210 CCAGCCCCCGTGCGGA-----AGTACAACTCC 3236 eCysAspileCysGiyCysPheAspLeuHisAspThrGluAspCysProThrGlnAlaGl 1393 -----CCC 3089 2307 GTCGACTATTCGGTCCTTCAGCAAAGATTTATG-----GAAGAAGAAACTAAGAAC 2357 2475 TCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGAGGAGGAGGAGCCCGGCT AAGAACATGGGGAGGAGGTCCTCAATCTG---ACCAAGGAGCTAGAGCTTTCCAAGCGC 2931 ATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCAAAAGTGCAGAGTCCTACTCTCGGC 2535 GIGITCATICGCAAAICCTICCAGGAGGAAAAICACAICATGAGIAAI------1244 ArgAsn------2358 2583 1262 1373 1246 1274 3087

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                                                                                                                                                                                                                                                                                                                                                   RY SEQUENCE OF 204-302 FROM N.A.

RY SEQUENCE OF 204-302 FROM N.A.

RY Adelstein Cortex;

RY TISSUB-Brain cortex;

RY Adelstein R.S.;

RT TWOUTONAL Cell expression of inserted isoforms of vertebrate nonmuscle myosin heavy chain II-8.;

RY TWO BIOL Chem. 270:1453-14540(1955).

CC -1- FUNCTION: Cellular myosin appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping (By similarity).

CC -1- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy capping subunits (MMC).

CC -1- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy capulatory light chain subunits (MMC) and 2 regulatory light chain subunits (MMC).

CC -1- SUBUNIT: The rodiike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha helical coiled coils.

CYCLES SIMILARITY: Contains 1 myosin-like globular head domain.

CC -1- SIMILARITY: Contains 1 lQ domain.

CC -1- SIMILARITY: Contains 1 lQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-RROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil;
Multigene family.

DOMAIN 785 MYOSIN HEAD-LIKE.

DOMAIN 786 815 IQ.
                                                                                                             16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, nommuscle type B (Cellular myosin heavy chain, type B) (Nommuscle myosin heavy chain-B) (NWMHC-B).
Bos taurus (Bovine).
Bukaryota; Mertazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Obaza M., Ishinagawa M.;
Host taurus nonmuscle myosin heavy chain B mRNA, complete cds.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                       PRT; 1976 AA
AATGCTAATATCATCACCACGGAAGACA 3264
                           1393 nMetLeuGluGluProProHisSerThr 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IRR000048; IQ_region.
InterPro; IRR001069; myosin head.
InterPro; IPR0010609; Myosin head.
InterPro; IPR002928; Myosin Lail.
InterPro; IPR002911; Spectrin.
Ffam; Pr00612; IQ; 1.
Pfam; Pr00612; IQ; 1.
Pfam; Pr01076; Myosin head; 1.
Pfam; Pr01076; Myosin Lail; 1.
Prints; Pr010193; Myosin Lail; 1.
PRINTS; PR00193; Myosin Lail; 1.
PRINTS; R000195; IQ; 1.
SWART; SM00115; IQ; 1.
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EMBL; U15716; AAA87715.1; -.
HSSP; P10587; 1BR2.
                                                                                       STANDARD;
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                                                                       BOVIN
MYHA BOVIN
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1052
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.092 uGlnGlyAlaLeuAlaArgGlyAspAspGluThrLeuHisLysAsnAsnAlaLeuLysVa 1112
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875 uGluGluMetGluArgLysHisGlnGlnLeuLeuGluGluLysAsnIleLeuAlaGluGl 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             895 nLeuGlnAlaGluThrGluLeuPheAlaGluAlaGluGluMetArgAlaArgLeuAlaAl 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 AGATGTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAGGCACACTA 415
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855 nålåLysAspGluGluLeuLeuLysValLysGluLysGlnThrLysValGluGlyGluLe
                                                                                                                                                                                                                                                                                                                                    AAGTTCATCTAACGGGCATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGATGGTGG
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229097 MW; 6144354451C0F790 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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40.93%
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5.71%
845 197(
178 18:
1976 AA;
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689 GGAGCGAGAG		uHishlalysval	13   13   13   13   13   13   13   13
3 6 6 6 6 6	3 6 8 6 8 6 8 6 8		86868686

1462 1783 1543 2012 2380 1501 1963 |::: ::::::||| |||::: 1543 uMetArgThrGlnLeuGluGluLeuGluAspGluLeuGlnAlaThrGluAspAlaLysLe 1563 2066 GAAGTICAGAACCGAGCAGGATAAGGCAAACTICCTCCCCAGCAGCTCGAGGAAATCAA 2125 ::: |||::: |||:::::||| 1582 rArgAspGluGlnAsnGluGluLysbysArgLeuLeuIleLysGlnValArgGluLeuGl 1602 2126 ACACCAAATGGCCAAGCACAAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCCGA 2185 2186 ACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCA 2245 2246 GGCTCTCAAGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCA 2305 ||||||| 1654 tLygAspTyr------GlnArgGluLeuGluGluAlaArgAlaSerArgAspGl 1670 1670 ullePheAljaGlnSerLyaGluSerGluLysLysLeuLysSerLeuGluAlaGlulleLe 1690 1667 CTTTAAGGTGGAGCAGGGAAAAGTCATGGATGTGACGGAA---AAGCTAATCGAGGAAAG 1723 1784 GAGGGATGAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAGAAGGTCCTGTGAACTGAGCTG 1843 1844 CAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGAGGTAGAAAGGGAAATAAA 1903 -----GIGGIGGAGGGGGACITGAIGAAGACCGAGGACGAAIAIGACCAGIIGGAGCA 2065 1634 uAlaAlaAsnLysAlaArgAspGluValIleLysGlnLeuArgLysLeuGlnAlaGlnMe 1654 2306 AGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGA-------2345 CAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGG 2440 | ||| ||| :::|||||| ||| ::: 1690 uGlnLeuGlnGluLeuAlaSerSerGlu-----ArgAlaArgArgHisAlaGl 1707 1616 GATGGAGAAAATAAAGCAAGAAGAGGGAAAGTGGGTTGG------AATAAAA 1666 2441 GAACGGCCGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGT 2500 2501 GTGCGGGGATGCTGCGGAGGAGGAGCCCCGGCTGTGTTCATTCGCAAATCCTTCCAGGA 2560 :::|||||| 1482 uThrLysAlaLeuSerLeuAlaArgAlaLeuGluGlu---AlaLeuGluAlaArgGluGl 1724 CAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGA -----GAAACTAAGAACAAGAACATGGGGAGGGCTCCT 1904 CCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGA 1964 ACTAACGCTTGAAATCGAGAGACTGAAAAACGGCTCCAGCAGTTGGAG------2561 GGAAAATCACATCATGAGTAATCTT 2585 ||||| | 1747 uGluGlnSerAsnMetGluLeuLeu 1755 1442 1538 2013 2381 g g g

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Search completed: September 7, 2004, 13:48:32 Job time: 275.5 secs

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Q968V1 rattus norvogosolo mus musculu Q8bdw1 mus musculu Q8bdw1 mus musculu Q8bdw1 mus musculu Q9fj35 arabidopsis Q9968 homo saplen Q8tbc7 plasmodium Q81hp3 plasmodium Q81h4 plasmodium Q81h4 plasmodium Q81h4 plasmodium Q07380 saccharomyc Q9nj22 aequipecten Q9nj21 aequipecten Q9nj21 aequipecten Q9nj21 aequipecten Q9nj21 aequipecten Q9nj21 aequipecten Q9nj23 aequipecten Q9nj23 aequipecten Q9nj24 mus musculu Q63731 rattus norvog2869 caenorhabdi Q9nj23 aequipecten Q9nj23 aequipecten Q9nj24 mus musculu Q83731 rattus norvog2869 caenorhabdi Q9nj23 aequipecten Q9vg484 drosophila Q8r384 mus musculu
                                                  Q81285 rattus norv
Q968K6 homo sapien
Q9nvis homo sapien
Q9cs72 mus musculu
Q8c872 homo sapien
Q8id20 homo sapien
Q8id397 homo sapien
Q85v48 homo sapien
Q8tehl homo sapien
Q8tehl homo sapien
Q95ng3 mus musculu
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O93522 xenopus lae
Q8ir55 drosophila
Q26080 placopecten
                    Q86tc3 homo sapien
Q9ule5 homo sapien
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagano T., Yoneda T., Hatanaka Y., Kubota C., Murakami F., Sato M.;
"Filamin A-interacting protein (FILIP) regulates cortical cell
migration out of the ventricular zone.";
Nat. Cell Biol. 4:495-501(2002).
EMBL; AB055759; BAC00851.1; -.
InterPro; IRF000933; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 1212 AA; 137752 MW; AlDSB9C5AF7D4F80 CRC64;
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Q727B0
Q86TC3
Q9ULE5
Q8JZS5
Q96SK6
Q9NVI8
Q9CS72
Q8N8B9
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QBLUM3
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QBFBH1
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QBCSL6
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Q26080
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MEDLINE=22100428; PubMed=12055638;
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Q8K4T4;
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   Command line parameters:
-MODEL=frame+.n2p.model -DEV=Xlp
-MODEL=frame+.n2p.model -DEV=Xlp
-DOSALIA 134021 10811/app query.fasta_1.4551
-DE-SCRTEMIL_25 -QFWT=fastan -SUFFIX=rspt -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -GTART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -GTART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USR=USIO98793 @CCAN 1 1 777 erunat 07092004 134021 10811 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPDRT=0.5 -FCAPDP=6
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                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                    - protein search, using frame_plus_n2p model
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Maximum Match 100%
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01-07T-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp451B134.
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WEDLINE=20039619; PubWed=10574462;

MEDLINE=20039619; PubWed=10574462;

Magase T., Ishikawa K., Kikuno K., Hirosawa M., Nomura N., Ohara O.;

The complete sequences of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from brain which code of 100 new cDNA clones from the code of 100 new cd the                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaTyrGlnAlaArgLy8GluLy8GluAsnAlaLy8ArgLeuAsnLy8Ly8ArgLeuArgAspGlu
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Momo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
VOBI_TaxID=9606;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein KIAA1275 (Fragment).
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Sciurognathi; Muridae; Murinae; Rattus
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MEDLINE=22100428; PubMed=12055638;
MEDLINE=22100428; PubMed=12055638;
MEDLINE=22100428; PubMed=12055638;
Megano T., Yoneda T., Hatanaka Y., Kubota C., Murakami F., Sato I Filamin A-interacting protein (FILIP) regulates cortical cell migration out of the ventricular zone.";
MAt. Cell Biol. 4:495-501(2002).
EMBL; D87257; BAGC08622.1; -.
InterPro; IFR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 965 AA; 109188 MW; 50352DF4F8236B40 CRC64;
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Q8JZS5;
Q8JZS5;
Q8JZS5;
Q1-OCT-2002 (TrEMBLrel. 22, Crea Ol-OCT-2002 (TrEMBLrel. 22, Last Ol-MR-2003 (TrEMBLrel. 23, Last Ellamin-interacting protein S-FILS FFILS PS-FILD Norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Cr Mammalla; Eutheria; Rodentia; Sc NEBI TaxID=10116;
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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6.3e-231
4838.00
100.00%
100.00%
62.58%
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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761 IleMetThrValSerThrSerAlaAlaProThrGluIleAlaValSerProGluSerGln 941 GluThrGlnSerMetLyglleGluLeuLygLygSerAlaAlaSerSerThrAlaSerLeu GAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACGAGGCCTGCATCCCCCATCCAA 3096 ATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCTGAATCTCAG 3216 CCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGACAATAAATTCAC 3636 GAGACTCAGTCTATGAAAATAGAGCTGAAGAAATCTGCAGCAGCAGCACTGCCTCTT 3576 GGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAATCTGACCAAATTCCAGCCTCGAGCT 2976 GATCCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGA 3276 ATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCA 821 IleHisLeuGlySerGlnPheLysArgSerProGlyProAlaAlaGluGlyValSerPro 3336 GTTATCACCGTCCGGCCTGTCAACGTGACAGGGAGAAGGAGGTTTCTACAGGCACAGTC 841 ValileThrValArgProValAsnValThrAlaGluLysGluValSerThrGlyThrVal 3456 ATAACTATAACCCCGGTCACAACGTCATCCACACGAGGAACCCAATCAGTGTCAGGACAA 921 GlyLysProValValAlaAlaSerGlyAlaGlyAsnLeuThrLysPheGlnProArgAla 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Hypotherical protein FL014799.
Homo sapiens (Human).
Bukaryota, Mertazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TTGAATAAAAACTTTAAGGTGGAGCAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATC ThrGluGlnAspLysAlaAsnPheLeuSerGlnGlnLeuGluGluIleLysHisGlnIle ACAAAGGAGAGGGATGAGCTGATGGGTAAACTGAGGAGGAAGAAGAAAGGTCCTGTGAA GAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAG ACCGAGGAGGATAAGGCAAACTTCCTCCCAGCAGCTCGAGGAAATCAAACACCAAATG AGGITTCGGCTGGAGGAGGCTAAAAGTCGTGAITTACAGGCCGAGGTGCAGGCTCTCAAG LysAlaGluLeuSerLeuLysAspAspLeuThrLysLeuLysSerPheThrValMetLeu GTGGATGAGAAAAAATATGATGGAGAAAATAAAGCAAGAAGAGAGGAAAGTGGATGGG CTGAGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGAGGTAGAAAGG ATCAGAGAACTAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTG GTGGAGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGA GCCAAGCACAAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACAC GAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTAT GluLysileHisGluLeuMetAsnLysGluAspGlnLeuSerGlnLeuGlnValAspTyr GCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCGGCTGTGTTCATTCGCAAATCCTTC CGGTCCTCGGTCCTCGACAGGTATCCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCT CAGGAGGAAAATCACATCATGAGTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAA

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1752 ATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGAGAGGATGAGCTGATGGGTAAACTGAGG 1811
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    OSNVIB PRELIMINARY; PRT; 653 AA.
OSNVIB CT-2000 (TrEMBLEEL 15, Created)
01-0CT-2000 (TrEMBLEEL 15, Last sequence update)
01-0CT-2000 (TrEMBLEEL 22, Last annotation update)
Hypochetical protein FLJ10708.
BURATYOTI, MCLEZOA; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eulbarya; Primates; Cararrhini; Hominidae; Homo.
NCBI_TAXID=9606;
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SEQUENCE 653 AA; 72451 MW; 33379801AD14AC86
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                                                                          CCCCTACACATCCGTGTGACACCAGATCATGAGAACAGCACTGCCACCCTGGAGATCACA
                                                                                     ProLeuHisIleArgValThrProAspHisGluAsnSerThrAlaThrLeuGluIleThr
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581 GlyThrGlnSerValSerGlyGlnAspGlySerSerGlnArgProThrProThrArgIle
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                                                           GGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCCCGGTCACAACGTCATCCACACGA
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
5730485H2IRIK protein (Fragment).
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuscullarxID=10090;
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MEDLINE=21085660; PubMed=11217851;
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PRINTS; PR00194; TROPOMYOSIN.
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 CTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAAGAACT 2351
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                                            GAGAGTCTGCGCAAGCGCGTGCTTGAGATGGAGGCCAAGGATGAAGAGATCACGAAGACC
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027860; AAH77860.1; -
SEQUENCE 893 AA; 102232 MW; 561BE17D6C10FDC4 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to downregulated in ovarian cancer 1.
Homo sapiens (Human)
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SEQUENCE FROM N.A.
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935 TOCANGOANGACCOCCANA CONTRICATION CONTRIC		Oy 2064 CAGAAGTTCAGAACCGAGCAGGATAAGGCAAACTTCCTCTCCCCAGCAGCTCGAGGAAATC 2123 :::::::::	OY 2124 AAACACCAATGGCCAAGCACAAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCC 2183	Qy 2184 GAACTGCGACACAGGTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTG 2243	2244 CAGGCTCTCAAGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTC	2304 CAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAACTAAGAACAAGAAC 	2364 ATGGGGAGGGAGCTCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCGGAGTS :::	<pre>Qy 2424 GCTCTCAGGCCGAGTGGGAAGGATGGTGACGTGCCTGTGGCCTCCACTGGG 2483 1::                                   </pre>	2484 GTGCAGACCGAGGCGT 	2532GCTGTGTTCATTCGCAAATCCTTCCAGGGGGAAAATCAC	OY 2571 ATCATGAGTAATCTTCGACGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTC 2630	2631GACAGGTATCCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCT	2676	2724 GAGAAAGGCCCAGGCCAAACCAGGGGCAGCACCCCGGGGAGCTGGTCCTAGCACCA :::	<pre>Qy 2784 AAGCAGGCCACCTACACATCCGTGACACCAGATCATGAGAACAGCACTGCCACC 2843                                       </pre>	2844 CTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTCTCTAGTACCACCGTCATT	OY 2898 CCTACCTTAGGCAACCAGAAACAGAATAACCATTATTCCATCACCAATGTCATGTGG 2957	Qy 2958 CAAAAGCCCAAAAGTGCAGATCCTACTCTCGGCCCAGAACGAGCCATCTCCCCTGTC 3014     Db 117 VallySerlySthrSerThrGlaspLeuMersanLeudludinglyMetSerProile 736     Ov 3015 ACGATTACTACTACTACTAGAGAAAAGTGGAAAGTTGGAAAGGAGGCCTTTGCCGAC 3074	
135 TCOARGOMGACCOCCAGAAGCTGCTOACTACTACATCAACAACAACAACAACACAAC		<u> </u>	<u>σ</u> α	<b>υ</b> α	<u> </u>	<b>σ</b> Δ	<u> </u>	<u>σ</u>	<b>σ</b> Δ		<u>о</u>	O A	O A	or a	o ñ	о ñ	0 0	o a 6	_
	TCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACACAAGGCCTCG :::   ::       :::	AGGTTTTCCCAGGACCACAAGACATGAACGCCAAATTGGCGAATCAAGAATCTCAAC :::	GGGAACTTCGACTCAAACTGGTTGGCTTATCGCAAGGATTGAGGAGCTGGAAGGACCTGGAAGGACCTGGAAGGACCTAACGAAGGATTGAGGAGCTGGAAGGACCTAATGGAAGAAAAAAAA			GAGATGGAGGCAAGGATGAAGAGATCACGAAGACCGAGGCCCAGTGCCGGAGCTGAAG ::	AAGAAGCTCCAAGAAGAACACCACAGCAAGGAACTTAGACTTAGAAGTGGAGAAGCTG    :::   :::	CAGAAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAGCGTTCAGCCGGAGTAAGTCGGAA	TGCACCCAGCTCCATCTGAACCTGGAGAAGAAGAACCTAACCAAAGACCTGAAC	GAGCTGGAGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAG 	AAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTG	GTGGATGAGAAAAATATGATGGAGAAAATAAAGCAAGAAGAGAGGAAAGTGGATGGG 	TTGAATAAAAACTTTAAGGTGGAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATC :::	GAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGAAAGGAGAGACTTGG       :::   :::	ACAAAGGAGAGGATGAGTGATGGGTAAACTGAGGAGGAGAAGAAGGAGGAGGAGAAGAAGTCCTGTGAA 	CTGAGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGAGGAGGTAGAAAGG	GAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCG	GAAGACAATAAGATCAGAGAACTAACGCTTGAAATCGAGAGCTGAAGAAAAAGGGCTCCAG	CAGTTGGAGGTGGTGGAGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAG

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ArgAspAspLeuLeuPheLeuLeuSerIleLeuGluGlyGluLeuGlnAlaArgAspGlu
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|SerAapGluPheIleCysLeuLeuGluGlnGluCysGluArgLeuLysLysLeuIleAap
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                                      GCCAATCGGAAGGAGGAG---GATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA
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| ArgThrMetSerProlleGlnValLeuAlaValThrGlySerAlaSerSerProGluGln
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| AppArgGinSerSerTrpGinPheGinArgSerAsnSerAsnSerSerSerVallleThr
                        AGGCCTGCATCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCCACTGAAATC
                                                                        GCTGTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCG
                                                                                                                       GAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACC
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TISSUE=Skeletal muscle;

Revert-Ros F., Raya A., Granero F., Saus J.;

"Cloning and expression of GIP90, a protein down-regulated in cancer "Cloning and expression of GIP90, a protein down-regulated in cancer submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF329092; AAN16206.1; -..

InterPro; IPR000533; TropOmyosin.

PRINTS; PR00194; TROPOMYOSIN.

SEQUENCE 764 AA; 89785 WW, DB41B4CB4EEFA085 CRC64;
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Catarrhini; Hominidae; Homo.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
GPBP-interacting protein 90.
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Matches:
Conservative:
Mismatches:
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                 ATCACGAAGACCGAGGCCCAGTGCCGGGAGCTGAAGAAGAAGAAGCTCCAAGAGGAAGAACAC 1319
                                                  CACAGCAAGGAACTTAGACTAGAAGTGGAGAAGCTGCAGAAGAGGATGTCTGAGCTGGAG 1379
                                                                                             1440 GAGAAGGAGAAGAACCTAACCAAAGACCTGCTGAAGGCTGGAGGTGGTCAAGAGTCGA 1499
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449 GluLysGluArgMetThrThrLysGlnLeuSerGlnGluLeuGluSerLeuLysValArg
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996 AGGTTTTCCCAGGAGCACGAAGAGATGAACGCCAAATTGGCGAATCAAGAATCTCACAAC 1055 GGGGAATGTGCAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGCGTGCTT 1235 816 ATGTTGGTGGACGAGGGCAGATGCACATCGAGCAACTGGGCCTGCAGAGTCAGAAAGTC 875 936 TCCAAGGAAGACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACAAGGCCTCG 995 876 CAGGACCTCACTCAGAAGCTGAGGAGGAGGAAGAAAAAACTCAAAGCGGTCACTTACAAA 81 ArgGlnLeuGlnGlnLysLeuAlaAlaAlaLeuSerArgGlnIleAspGluLeuGluGluThr CGGCAACTICGACTCAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAAGAGACC Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; SEQUENCE FROM N.A. MEDLINE-94148289; PubMed=8314147; Mok S.C., Wong K.K., Chan R.K., Lau C.C., Tsao S.W., Knapp R.C., Berkowitz R.S.; "Molecular cloning of differentially expressed genes in human epithelial ovarian cancer "; molecular cloning of differentially expressed genes in human epithelial ovarian cancer "; [1] Cylosol. Oncol. 52:247-252 (1994). [2] SEQUENCE FROM N.A. WONG K.K., Mok S.C.; WONG K.K., Mok S.C.; Submitted (AFR-1996) to the EMBL/GenBank/DDBJ databases. Submitted (AFR-1996) to the EMBL/GenBank/DDBJ databases. GOJ, GOJ.0016459; GIMYOSI, NAS. SEQUENCE 752 AA; 87141 MW; D763B4E2806A3B0B CRC64; Created) Last sequence update) Last annotation update)

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SerLeuArgProSerLeuAsnGlyArgArgIleSerAspProGlnValPheSerLysGlu
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1701 ACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGGAA 1760
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------AsnArgAspTyrThrArgAsnAlaSerAsnLeuGluArg
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----AspSerGlyThrGlnGluThr
                            1581 TTCACTGTGATGCTGGTGGATGAGGAAAAATATGATGGAGAAAATAAAGCAAGAAGAG
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       AAAGACCTGCTGAACGAGCTGGAGGTGGTCAAGAGTTAAAGAACTCGAATGCTCC
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265 LysGlnValGluAsnGluThrArgAsnLysSerGluAsnGluLysAsnArgAsn----
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435 SerHisMetGlyValSerThr--
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TISSUE=Testis;

XX BEDINE=2138855;
    PubMed=12477932;
    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
    Alschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
    Alschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Haich N.K.,
    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich N.K.,
    Blatchins L.M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
    Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
    Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
    Brossk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
    Bosak S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
    Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
    Bukesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
    Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
    Jones S.J., Marra M.A.;
    Jones S.J., Marra M.A.;
    Jones S.J., Marra M.A.;
    Jones C., Grimwood M., Rodrigues R.M., Butterfield Y.S.,
    Jones S.J., Marra M.A.;
    Jones C.M. Schmerch A., Schein J.E.,
    Jones C.J., Marra M.A.;
    Jones M. J., Marra M.A.;
    Jones M. J., Marra M.A.;
    Jones M. J., Marra M.A.;
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ArgGinArgValLeuArgIleGluGlyLysAspGluGluIleLysArgAlaGluAspLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. BMBL, BCO61733, AAH51733.1; -. GO; GO:0005743; C:mitochondrial inner membrane; IEA. GO; GO:0006810; P:transport; IEA. GO; GO:0006810; P:transport; IEA. InterPro; IPRO0193; Mitoch carrier. PROSITE; S00215; MITOCH CARRIER; I. SEQUENCE 1026 AA; 114616 MW; A8A11163CB24DF5A CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
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Pred. No.:
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    780 LysGlnLysProValSerLysProGlyProAsnLysValThrSerSerlleThrIleTyr 799
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                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1046 AA; 116695 MW; 2942129B20048C7F CRC64;
                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK074153; BAB84979.1; -.
HSSP; P04268; 11C2.
                                                                                                                                                                                                                                                                                       Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., "The nucleotide sequence of a long cDNA clone isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1046
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GO; GO:0005743; C:mitochondrial inner membrane; IEA.
GO; GO:0005488; F:blaiding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001993; Mitoch carrier.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                Length:
Matches:
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                          3.63e-36
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47.86%
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                                                                                                       PRELIMINARY;
                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                                                                                                                                                                                         TISSUE=Spleen
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3108 AGGAACCACCTCTTCAAGACCCGGTGCTAGCAAGTGACCAGCACTATAACTATAACC, 3467
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-----ABpLyBABpValLyBLyBIleMetGlyGlySerGlyThrGluThrThrLeuGlu 779
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535 SerĞluThrValPheGly---LysArgGlyHisValLeuGlyAsnGlySerGlnValThr
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                                                                                        2652 AATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAGAGAAAACGGTCCT
                                                                                                                GlnGluHisSer-----LysAlaTrp------LysGlyThrSerLysPro
                                                                                                                                                                     495 GlyThrGluSerGlyLeuLysGlyLysValGluLysThrThrArgThrPheSerAspThr
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2532 GCTGTGTTCATTGGCAAATCCTTCCAGGAGGAA  442	3363 ACAGCGGAGAAGAGGGGTT
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122 ArgSerLyabanAspCyathrOlnLeucysLeuserLeukanGluGlukryabanLeuThr 141   1461   AAAGACCTOCTGAACGAGGTCAACGTC	2472 GCCTCCACTGGGGTGAGGCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCG 2531 :::
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2532	GCTGTGTTCATTCGCAAATCCTTCCAGGAGAAAATCACATCATGAGTAATCTTCGACAG 2591
2592 456	GTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGTATCCCCCAGCAGG 2651
2652	AATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGAT 
2712	TCCACT
48	GlyThrGluSerGlyLeuLysGlyLysValGluLysThrThrArgThrPheSerAspThr 507
2718	
2763	GGGGA     SerG1
2817	CCAGATCATGAGAACAGCACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAGATTT 2876
2877	
2937	
2973	GCAGATCCTACTCTCGGCCCAGAAGGAGC GCAGAT-CTCTCGGCCCAGAAGGAGC  CYSATGSerGlnGluAsnIleLeuGlnGlyPheSerThrSerHisLysGluGlyVa
3006	TCCCCTGTCACGATTACTACTATTTCCAGAGAGAAGAGCCCGGAAGGTGGA
3057	
3099	ATGACGGT    SerLeuVa
3159	GTGCCTATGGGAAGGACTATCCTCAAAGTCACCCGGGAAAACAAAC
3207	
3246	ATCATCACCACGAAGACAATAAAATTCACATTCACCTGGGTTCTCAGTTTAAGCGA 3302 :::         :::         ::: ThrMetGlubeuProAspThrAsnGlyAlaGlyValLysSerGln 734
3303	TCTCCTGGGGCCTGCGGCTGAGGGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTG 3362
3363	ACAGCGGAGAAGGAGGTTTCTACAGGCACAGTCCTTCGCTCCCC 3407 :::   :::   :::

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AGGAACCACCTCTCTTCAAGACCCGGTGCTAGCAAAGTGACCAGCACTATAACTATAACC 3467
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LysGlnLysProValSerLysProGlyProAsnLysValThrSerSerIleThrIleTyr
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                            Chang N.C.;
"Identification, molecular characterization, and chromosomal localization of the cDNA encoding a novel leucine zipper motif-
                                                                                                                                                                                                                                                                  Sun D.S., Chang A.C., Jenkins N.A., Gilbert D.J., Copeland Chang N.C.,
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839.00
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Genomics 36:54-62(1996).
EMBL; L49344; AAA98795.1;
HSSP; P04268; 1IC2.
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-----LeuArglleGluAspGlylleSerSerThrLeuSerSerLysGluSerLysArg
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8 ; Search time 2349 Seconds (without alignments) 7892.353 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Acc45354 Rat L-FIL
Acc45355 Rat S-FIL
Adb49155 Novel hum
Aai59172 Human pol
Acc45356 Human L-F
Aah14619 Human cDN
Ach3929 GPBP-inte
Acc3930 GPBP-inte
Acc393 Human cer GPBP-inte Human pro ben Human Description Abz71968 H Acf12851 H Acc83934 G Aaf22838 H SUMMARIES ACC83929 ACC83930 ACC83927 ACC90628 ABZ71968 ACF12851 ACC83934 AAF22838 ACC45354 ACC45355 ADB49155 ACC83928 AAH06919 ABK35549 **ABK64739** AAH14619 ACH03975 AAH06432 AA160958 AA159172 ACA04011 ACC45356 В Length 46892 3554 25594 2402 34115 3430 3998 3587 3025 3025 3025 3025 2355 1241 844 1326 Query Result

Acc83926 GPBP-inte	Acc83925 GPBP-inte	Aaf18033 Lung canc	Adc30104 Human nov	Abq77428 Human CGD	Acf34447 Gene enco	Adb63229 Human cDN	Aaf22892 Human pro	Aaf22947 Human pro	Acc83940 GPBP-inte	Acc83924 GPBP-inte	Aas33804 Human cDN	Aai21417 Probe #11		Aba48586 Human bre	Aba33560 Probe #12	Aak40654 Human bon	Human	Abs40222 Human liv	Aai07111 Probe #71	Aah11941 Human cDN	Acc83941 GPBP-inte
ACC83926	ACC83925	AAF18033	ADC30104	ABQ77428	ACF34447	ADB63229	AAF22892	AAF22947	ACC83940	ACC83924	AAS33804	AAI21417	AA146706	ABA48586	ABA33560	AAK40654	AAK14921	ABS40222	AAI07111	AAH11941	ACC83941
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292	265.4	248.2	240.6	240.6	240.6	239.8	231.4	212.6	204.4	202.8	195.2	182.8	182.8	182.8	182.8	182.8	182.8	182.8	182.8	177.2	154
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## ALIGNMENTS

Proteins controlling cell migration and cell death and their encoded DNAs, applicable in developing drugs for treating or suppressing cancer or tumor metastasis or as regulators of cell migration for L-FILIP, S-FILIP, filamin-interacting protein; cell migration; cell death; cytostatic; neuroprotective; immunosuppressive; cancer; tumour metastasis; transplantation therapy; gene; ss. 75. .3713 /\*tag= a /product= "L-FILIP" /note= "filamin-interacting protein" Rat L-FILIP encoding cDNA SEQ ID NO:1. (NISC-) JAPAN SCI & TECHNOLOGY CORP. Claim 2; Page 45-54; 96pp; Japanese. Location/Qualifiers BP. ACC45354 standard; cDNA; 4364 29-JUL-2002; 2002WO-JP007676. 27-AUG-2001; 2001JP-00256910 (first entry) WPI; 2003-268423/26. P-PSDB; ABP97029. Sato M, Nagano T; norvegicus WO2003018804-A1 transplantation 18-JUN-2003 06-MAR-2003 ACC45354; Rattus Key RESULT 1 ACC45354 

The present sequence encodes rat L-FILIP which is a filamin-interacting protein. L-FILIP has a function of controlling cell migration and cell

ACATCGAGCAACTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCACTCA	1081 GCTTATCGCAAAGGATTGAGGACTGGAAGACCCATAAAAGCCTTCACAAGGCGAGGG	TCACGAAGTGGAGAGTCTGCGCAGAGCGCGTGCTTGAGATGGAGGCAAGGATGAAGAGA TCACGAAGACCCAGGCGCAGCGCGGGAGCTGAAGAAGAAGCTCCAAGAAGAAGAACCC	1321 ACAGCAAGGAACTTAGACTTGCAGAAGAGGAGGATCTGCAGAGATCTGCAGAGATCTGAGATA 1380  1381 AGCTGGAGGAACTTCAGCCGGAGTAAGTCGGAAATGCACCCAGGTCCATCTGAACCTGG 1440  1381 AGCTGGAGGAAGGATCAGCCGGAGTAAGTCGGAATGCACCCAGGTCCATCTGAACCTGG 1440  1381 AGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTGAACCTGG 1440	1441   AGAAGGAGAACCTAACCAAAGACCTGCTGAACGAGCTGGTGGTCAAGAGTCGAG   1500	1561 ACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGAAAAATATGATGG 1620	AGGGAAAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAACAAGAAGCTTTTAAAAC	1/41 TCAAATCTGAAGGGGAGGGAAGAGGAGTACGGTCTGACAAGGGAGGG	1861 AGAAGCGGCTTGATGGGGATAGAGGAGGTAGAAAGGGAAATTAACCGAGGTAGGT
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CC death. L-FILIP has cytostatic, neuroprotective and immunosuppressive CC activities. The L-FILIP protein can be used for controlling cell CC migration and cell death, which is applicable in developing drugs for CC treating or suppressing cancer or tumour meterastasis or as requiators of CC cell migration for transplantation therapy, and also for controlling the CC mobility and cell death of nerve cells, promoting decomposition of the CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein in the treatment CC actin-binding protein e.g. filamin-interacting protein e.g. filamin-interacting e.g. filamin-interactin	QY         1 CCACTGGGTTCTTCAAGGGATAAACCAGGGGGGAAAGAACACACCATTGGTTAAGGAGTC 60           Db         1 CCACTGGGTTCTTCAAGGATAAACCAGCGGGAAAGAACACACCATTGGTTAAGGAGTC 60           QY         61 GACAACAGGTGGGAATCACGAAATCAAGGTGGAGAAAGTTCATCATCAACGGGCATG 120           Db         61 GACAACAGGTGGGAATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCATCTAACGGGCATG 120           Db         61 GACAACAGGTGGGAATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCATCATCAACGGGCATG 120	121 TCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGATGGTGAGGGCCCCTCAGAAGATG 121 TCTCTGCCCCCAAGTCCTCCATCATCAGGAGTAAGGGCCCCCTCAGAAGATG 121 TCTCCTGCCCCCAACCTCATCATCAGGATGATGGTGATAAGGGCCCCTCAGAAGATG 181 CAAAAAGAACAAGGCCAATCGGAGGAGGAGGTGTCAGGATTCCAGAAAAGAACAAGGCCAATCGGAAGAGGAGGAGGATGTCATGGCTTCCGGAACTATCAAAA 181 CAAAAAAGAACAAGGCCAATCGGAAGGAGGAGGATGTCATGGCTTCCGGAACTATCAAAA	27 21 0000000000000000000000000000000000	361 TCATCCACATGCTGAGGACAGAGAAACCAAGCCCGAGGTTCTGGAGGCACATGGAT	1	Db   541 AGCAGAAGAGAGACGTACCGCGCATAGCTAGAGCAGCTGCTGGAGAAGTGTCACA 600		Oy 781 GAGATGAGCTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGAGAGGCAGATGC 840

CCGGGGGGCTGCTCCTAGCACCAAAGCAGGCCAGCCCTACACCTCCGTGTGACACCAG AAGAAGAAACTAAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCTAG ATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGTATC CCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAGAG AGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGG AAAACGGTCCTTCCACTCCGCAGGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACC ATCATGAGAACAGCACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTCT

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997 GGTTTTCCCAGGAGCACGAAGAGATGAACGCCAAATTGGCGAATCAAGAATCTCACAACC 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins controlling cell migration and cell death and their encoded DNAs, applicable in developing drugs for treating or suppressing cancer or tumor metastasis or as regulators of cell migration for transplantation.
                                                                                                                                                                                      4261 AAACAAAAGCCCCTAATATGACCTCAGGAAACAATTTGAACATGAAATAAAATG
                                                                     ATATGGGTTATAAGAAAAGAATACTTTCAGAGCTATCACAGGGTCTCTAAAACTTTTGGAA
                                                                                                 ATATGGGTTATAAGAAAAGAATACTTTCAGAGCTATCACAGGGTCTCTAAACTTTTGGAA
                                                                                                                                                            AAACAAAAGCCCCTAATATGACCTCAGGAAACAATTTGAACATGAAATTGGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-FILIP; S-FILIP; filamin-interacting protein; cell migration; cell death; cytostatic; neuroprotective; immunosuppressive; cancer; tumour metastasis; transplantation therapy; gene; ss.
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                                                                                                                                                                                                                                               /product= "S-FILIP"
/note= "filamin-interacting protein"
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The invention relates to a polynucleotide comprising a sequence given in the specification, or its mature protein-coding portion, or its complement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Note: The sequence data for this patent did not form part of the printed as specification but was obtained in electronic format directly from USPPO at sequence.html?DocID=20030104529.
                                                                                                                                                                                                                                                                                                                                 59 TCGACAACAGGTGGGAATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCA
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                                                                                                                                                                                                                  Query Match 69.3%; Score 3025.6; DB 8; Length 4892; Best Local Similarity 82.5%; Pred. No. 0; Matches 3593; Conservative 0; Mismatches 734; Indels 27;
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                         GAAGATGTTGGTCCAGTTCAGTTTTACTTCTAGCATGTGGCCCCATTCAAGGTAGCTCAC 3996
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25-APR-2000; 2000US-00552317.
19-JUL-2000; 2000US-00620312.
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1976 AATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGACTTGATGAA 2 2538 AATTGAGAGACTGAAGAACGTCTCCAACAATTGGAAGTGGTCGAAGGGGACTTTGATGAA 2 2036 GACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAAGACGAAGCGAAGCGAATTTGATGAA 2 2598 GACCGAGGAATATGACCAGTTGGAGCAGAAAGTTTCAAGATAAGGCAAA 2 2598 GACAGAAGATAGACTGAGAAATCGAAAATTTAGAACTGAGCAAAAGCCTAA 2	CTTCCTC CAAAGGG GAAGGGT GAAGGGT TABBBBGT		2898 TATGGAAGAAATAAACAAAACATGGGGGAGGGGTCTCTCAATCTGACCAAAGA 2 2396 GCTAGAGGGTTACAAGGGGTACAAAACATGGGGGCGAGGGGTTCTCAATCTGACCAAAGA 2 2396 GCTAGAGGGCTACAGGGGTACAGGCGAGTGCAAGGGAT 2 2958 GTTGGAAGGGTTACAAGGGCTACAGGGTGTTAGGCCCAGTGAATGAA	3018 GGTGGATGTTCCTGTGACGTCAACTGAAGCTGATGAGGGGTAAAGCAGG 2516 GGAGGAGGAGACCCCGGCTGTGTTCATTCGCAAATCCTTCCAGGAGGAAAATCAT 2 2516 GGAGGAGGAAGAACCCCGGCTGTGTTCATTCGCAAATCCTTCCAGGAAAATCACTAT 2 3078 AGAGGAAGAAAACGCCAGCTGTATTCATACGGAAATCCTTCCAGGAAGAAATCATATTAT 3 2576 GAGTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAG 2 2576 GAGTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAG 3 3138 GAGTAATCTTCGACAGGTAGGCATTGAAGAAACCCGTGGAAAGATCTTCTGTTCTAGACAG 3	2636 GTATCCCCCAGCAGATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAA 2 3198 GTATCCTCCAGCAAATGAGCTCACTATGAGAAGTCTTGGATTCCATGAGAAA 3 2696 AAGAGAAAACGGCACAATGAGCTCACTATGAGAAGTCTTGGATTCCATGGATGAGAAA 3 2696 AAGAGAAAACGGTCCTTCCACTCCGCAGGAAAAGGGCCCAGGCCAAACCAGGGTGCAGG 2 1	2756 GCACCCGGGGAGCTGGTCCTAGCACGGGGCCAGCCCTACACATCCGTGTACACATCCGTGTGAC 2	2876 TITCTCTAGTACCACCGTCATTCCTAGGCAACCAGAAACCAAGAATAACCATTAT 2 3438 TITTCTGTAGTACCACTGCTTAGGGAATCAGAACCAAGAATAACCATTAT 3 2936 TITTTCTAGTACCACTGTCATTCTACCTAGGGAATCAGAACCAAGAATAAACATTAT 3 2936 TCCATCACCAACCATTATGCTCACAAAGTGCAGATCCTACTCTGGCCCAGA 2 11
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	1016 AGAGATGAACGCCAAATTGGCGAATCAAGAACTCACAACCGGCAACTTCGACTCAAACT 1075	1136 AGAGGAAGAGCTCCAGGAGCTGAGAGAAATTGCCAAAGGGGAATGTGGAAACTCCAG 1195	1256   AGGARGACGARGACCGAGGCGGGGGAGAGAGAGCTCCAAGAGGAAGA   1315   1		2058 TCGAGTTAAAGAATTGGAATGTTCTGAAAGTAGATTGGAAAAGCCTGAATTAAGCCTAAA 2117  1556 AGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGGGAGGGA		

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1194 GTTTGATATATGGGTTATAAGAAA-AGAATACTTTCAGAGCTATCACAGGGTCTCTAAAC 4252
                                                                                  1739 ATTTGCTTTATGTGCTGGAAAAACATCACATAGCTATCACAGGGCCTGGACCTCTAAAA 4798
                                                                                                                 4253 TTTTGGAAAAACAAAAGCCCCTAATATGACCTCAGGAAACAATTTGAACATGAAATAAAA 4312
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immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                Human, nootropic, immunosuppressant; cytostatic; gene therapy, cancer peripheral nervous system; neuropathy, central nervous system; CNS; Alzheimer, s, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Yang Y,
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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21-JAN-2000; 2000US-00489725.
25-APR-2000; 2000US-0055317.
20-UN-2000; 2000US-00589042.
19-UUL-2000; 2000US-0058912.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-0065319.
19-CT-2000; 2000US-0053036.
29-NOV-2000; 2000US-00727344.
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                     3738 AATCCTCAAAGTCACCCCAGAAAAACAGACTGTTCCAACTCCAGTACGGAAATACAACTC 3797
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lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes human L-FILIP which is a filamin-interacting protein. L-FILIP has a function of controlling cell migration and cell death. L-FILIP has cytostatic, neuroprotective and immunosuppressive activities. The L-FILIP protein can be used for controlling cell migration and cell death, which is applicable in developing drugs for treating or suppressing cancer or tumour metastasis or as regulators of cell migration for transplantation therapy, and also for controlling, the mobility and cell death of nerve cells, promoting decomposition of the actin-binding protein e.g. filamin-interacting protein in the treatment of preiventrilcular nodular heterotopia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins controlling cell migration and cell death and their encoded DNAs, applicable in developing drugs for treating or suppressing cancer or tumor metastasis or as regulators of cell migration for
                       GTTTGATATATGGGTTATAAGAAA-AGAATACTTTCAGAGCTATCACAGGGTCTCTAAAC
                                             ATTTGCTTTATGTGCTGGAAAAACATCACATAGCTATCACAGGGCCTGGACCTCTAAAA
                                                                     TTTTGGAAAAACAAAGCCCCTAATATGACCTCAGGAAACAATTTGAACATGAAATAAAA
                                                                                            TTTTGCAAAAACAAAAGGTTCTAAGATGATTTCAGGAAATAATGTGAACATGTAATAAAA
                                                                                                                                                                                                                                                                                               L-FILIP, S-FILIP, filamin-interacting protein, cell migration, cell death, cytostatic, neuroprotective, immunosuppressive, cancer; tumour metastasis; transplantation therapy, gene; ss.
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                                                                                                                                                                                                                                                                          Human L-FILIP encoding cDNA
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P-PSDB; ABP97031.
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CCTGGGCCTGCCGCTGAAGGCGTGAGCCCCAGTTATCACCGTCCGGCCTGTCAACGTGACA
                        GCGGAGAAGGAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGGAACCACCTCTTCA
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

[a] an oligo-dr primer and an oligonucleotide comprisentary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 5'-end
complementary strand of a polynucleotide which comprises a 1'-end sequence, where the
complementary strand of a polynucleotide complementary to a
coligonucleotide comprises a 1'-end sequence, where the
colification The primer sets can be used in antisense therapy and in
complementary full-length cDNAs. The primers are also useful for the
chetction and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
convas easily without any specialised methods AAH03166 to AAH13628 and
AAH13631 to AAH13632 represent human cDNA sequences; AAB92446 to AAB95893
crepresent human anino acid sequences; and AAH3632 represent
complementary sequences; and sequences; and sequences; and complementarion of the
                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                          therapy;
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                                                                                                                                                                                          therapy; gene
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Otsuki
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A, Nagai K,
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                    AAH14619 standard; cDNA; 3558
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11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-002418997.
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Ishii S, Sugiyama T, Wakama
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AAH14619
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GAAAATGCTAAACGACTCAATAAACTAAGAGATGAGCTTGTTAAACTCAAATCCTTTGCA

GAAAACGCTAAGCGGCTCAACAACTTCGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCC

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Best Local Similarity Matches 2917; Conserv

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Human cDNA sequence SEQ ID NO:11923.
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
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GGAGATACTACTTGGCCCAGAACGAGCCATGTCCCCAGTCACAATTACTACATTTCC
                          CAGATAATGACGGTGTCTACATCAGCAGCACCAGCTGAGATTGCAGTTTCTCCCCGAATCC
                                                                                                CAAATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCT
                                                                                       GCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGACAATAAAATT
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The present invention describes primer sets for synthesising 5602 full-
length CDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polymucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polymucleotide which comprises a 5'-end
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a polymucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 1'-end sequence, where the
complementary strand of a polymucleotide and the combination of
complementary strand of a polymucleotide and the combination of
complementary strand of a polymucleotide which comprises a 1'-end sequence is selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
gene therapy. The primers are useful for synthesising polymucleotides,
complementary full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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CTGTGAT-TTTTTTTCCAAAAAAAAAATATTTTGAAATAGGACAGAGTTTAACAGTTGT
                                                                                             3341 CCACAATAATTTTTTATTAAAAAAATCCTATTACAAAATAAGACATACTTTAACTATTGT
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Sugiyama T, Wakamatsu A, Nagai K,
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TCTTCTTCTTAGACAGGTATCCTCCAGCAGCAAATGAGCTCACTATGAGAAAGTCTTGG
                                                              CTACACATCCGTGTGACACCAGATCATGAGAACAGCACTGCCACCCTGGAGATCACAAGC
                                                                                                                                           CTGCATATTCGAGTGACACCAGGAGAAACAGCACTGCGACTTTGGAGATAACAAGC
                                                                                                                                                                     CCCACATCTGAAGAGTTTTTCTCTAAGTACCACCGTCATTCCTACCTTAGGCAACCAGAAA
                                                                                                                                                                                    CCGACATCTGAAGAATTTTTTTTTTTTTTTTCTAGTACCACTGTCATTCCTACCTTAGGGAATCAGAAA
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detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3331 to AAH1872 represent human cDNA sequences, AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent cliquouclectides, all of which are used in the exemplification of the present invention
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                                                                                                 Length 2594;
                                                                                Sequence 2594 BP; 869 A; 555 C; 580 G; 590 T; 0 U; 0 Other;
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                                                                                                 Score 1729.4;
Pred. No. 0;
0; Mismatches
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Local Similarity 80.8%;
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                                                                                                                                            complements that are differentially expressed in respiratory disorder. The combination is useful for preparing a composition for diagnosing or treating respiratory disorders e.g. lung cancer, chronic obstructive pulmonary disease, emphysema or acthma. The present sequence represents human cDNA differentially expressed during lung cancer
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             New combination comprising cDNAs that are differentially expressed in réspiratory disorders, useful for diagnosing or treating respiratory disorders e.g., lung cancer, chronic obstructive pulmonary disease,
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                              The invention relates to a combination comprising cDNAs or their
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                                                                                                                                                                                                                                                                              Length 2402;
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Pred. No. 0;
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The present full-length cDNA sequence encodes GIP130b, a novel 130 kDa Goodpagture antigen binding protein (GPBP) interacting protein. The CDNA was isolated from a skeletal muscle cDNA library. The DOC/GIP90/130 mRNA family results from a complex diversification mechanism operating on the expression of the GIP90 gene on chromosome 3 (3q12). GIP90/130 on the polypeptides of the invention interact with GPBP and are capable of aggregation. They can be used to modify GPBP-GIP90/130 interactions, to modify GP90/130 aggregation, and to modulate gene expression. The invention provides GIP90/130 polypeptides, portions of them, antibodies, nucleic acid sequences, expression vectors and host cells, as well as methods for detecting GIP90/130 polypeptides and nucleic acids, and methods for treating an autoimmune disease or cancer by modifying the expression or activity of one or more GIP90/130 polypeptides New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or Page 73-78; 115pp; English 48; Claim 

Sequence 3415 BP; 1293 A; 691 C; 758 G; 673 T; 0 U; 0 Other;

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1365 1305 1461 2013 1101 1701 2073 921 TGAAATGCAATTTAGAAAAGAAAGGATGACCACAAAGCAGTTGTCTCAAGAACTGGAGA AGCTTCAAGTGGAGCAAAATAAAGTAACAACAGTTACTGAGAAGTTAATTGAGGAAACTA 1822 aaaacaaattaaatcaagactctgggaaatccacaagagtatacaccaagaaaacaata GACTCAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAAGAGACCAATAAAAGCC GCAAGGATGAAGAGATCACGAAGACCGAGGCCCAGTGCCGGGAGCTGAAGAAGATCCC GGAAAGATGAAGAGCTCATAAAAATGGAGGAGCAGTGCAGAGATCTCAATAAGAGGCTTG <u> aaagggagacgttacagagtaaagactttaaactagaggttgaaaaactcagtaaaagaa</u> TTATGGCTCTGGAAAAGTTAGAAGACGCTTTCAACAAAAAGCAAACAAGAATGCTACTCTC TGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGT TAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGA TCACTCTAAAAGAGATTTTAACTAAACTGAAAACATTAACTGTGATGTTTGTAGATGAAC GGAAAAATATGATGGAGAAAATAAAGCAAGAAGAGGAGGAAAGTGGATGGGTTGAATAAAA GTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGAGGTAGAAAGGGAAATAAACC GAGTTAATATGTTGAAAAATAGGCTTCAATCATTGGAAGCAATTGAGAAAGATTTCCTAA AGATTAAGGAGCTCTCTCAAGAAGTGGAAAGACTGAAACTGAAGCTAAAGGACATGAAAG TGGTGGAGGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCA AGGAGCACGAAGAGATGAACGCCAAATTGGCGAATCAAGAATCTCACAACCGGCAACTTC AACAAAAGCTGGCAGCACTCAGCCGGCAGATTGATGAGTTAGAAGAGACAAACAGGTCTT TTCAGAAGGCAGAGGAAGAGCTCCAGGAGCTGAGAGAGAAAATTGCCAAAGGGGAATGTG Tacgaaaaacagaagagagctgcaagatataaaagaaaaaatcagtaaggagagaatatg GAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGCGTGCTTGAGATGGAGG GAAACGCTGGTATCATGGCTGAAGTGGAAGAGCTCAGGAAACGTGTGCTAGATATGGAAG AAGAGGAAGAACACCACAGCAAGGAACTTAGACTAGAAGTGGAGAAGCTGCAGAAGAGA TCCATCTGAACCTGGAGAAGGAGAACCTAACCAAAGACCTGCTGAACGAGCTGGAGG GTTTAAAAGTAAGGATCAAAGAGCTAGAAGCCATTGAAAGTCGGCTAGAAAAGACAGAAT ggaaaacaargaagaaaaarraaagaaaacrgaagaraaarracaagcrgcrrcrrcr ACTITAAGGTGGAGCAGGGAAAAGTCATGGATGTGACGAAAAGCTAATCGAGGAAAGCA AGAAGCTTTTAAAACTCAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGA <u>APAGGGCGCTCAAGTCCAAAACCGATGTAGAAGAAAAGATGTACAGCGTAACCAAGGAGA</u> GGGATGAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAAAAGGTCCTGTGAACTGAGCTGCA GAGATGATTTAAAAAACAAATTGAAAGCGGAAGAAGAAAGGAAATGATCTCCTGTCAA GAGGTAGGTCGTGCAAGGGGTCTGAGTTCACC-------TGCCCGGAAGACAATA AGATCAGAGAACTAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGG 1066 1546 1042 1186 1102 1246 1306 1366 1426 1342 1486 1462 1606 1666 1726 1762 1906 862 1006 922 982 1126 1162 1282 1402 1522 1582 1642 1786 1702 1846 셤 셤 요 g g a a g g g g g 8 & ð ò ò ò ઠે ò ò ò 셤 ð 셤 ð g à ò 셤 8 셤 ò ò 셤 Š

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                                                                                                     3070 cagaaccaacagaarcagraccaagcargcgararrcagagrcrcccagaccggcagr
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379 Trcaagcaaaarcracccrragcaagaagacarcratcratgadaaccaargaardagrrag 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present full-length cDNA sequence encodes GIP130a, a novel 130 kDa Goodpasture antigen binding protein. (GPBP) interacting protein. The CDNA was isolated from a skeletal muscle CDNA library. It represents an mRNA species that results from faithful transcription and translation of GIP90 genomic DNA. GIP90/130 polypeptides interact with GPBP and are capable of agrecation. They can be used to modify GPBP-GIP90/130 interactions, to modify GP90/130 aggregation, and to modify GPBP-GIP90/130 interactions, to mivelence provides GIP90/130 polypeptides, portions of them, antibodies, nucleic acid sequences, expression vectors and host cells, as well as methods for detecting GIP90/130 polypeptides and nucleic acids, and methods for detecting an autoimmune disease or cancer by modifying the expression or activity of one or more GIP90/130 polypeptides
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                             GIP130a;
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Local Similarity 55.2%; Pred. No. 2.1e-174;
es 1679; Conservative 0; Mismatches 1329; Indels 33;
                       Goodpasture antigen binding protein interacting protein; GPBP; human; transcription factor; autoimmune disease; cancer; immunosuppressive; cytostatic; chromosome 3q12; gene; ss.
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GPBP-interacting protein GIP130a coding sequence.
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                                                                                                                                    Location/Qualifiers
9. .3416
/*tag= a
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20-MAY-2002; 2002US-0382004P.
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REVERT-ROS F.
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                             AGGGATCTGTGCTGCTTCAAATGCAGCCAGTCTACTCCATGTCCTGTTAACAGAAAGC
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         AGGICCICAAICIGACCAAGGAGCIAGAGCITICCAAGCGCTACAGCCGAGCICTCAGGC
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1519   GGAAAACAATGAAAAATTAAAGAAAACTGAAGATAAATTACAAGCTGCTTCTTCTC   1578   166   ACTTTAAGGTGGAACAGGAAAAGTCATGGATGACGAAAAGCAAAGGAAACTA   1726		2014 TGGTGGAGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCA 2073  1939 CCATTGAGGATGACAGAAGAGGAGGATGAATTGAGACTCTAGAAGGTATG 1998  2074 GAACCGAGCAGGATAAGGCAAACTTCCTCCCCAGCAGGTCTAGAACGAAAGGTATG 1998  2074 GAACCGAGGAGAAAGCTAGCAAACTTCCTCCCCAGCAGGAAATCAAACAAA	ACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGTCTCA	2314 ATTCGGTCCTTCAGCAAAGATTATGGAAGAAAACTAAAGAACATGGGGAGGG 2373 2236 ACTCAGTCCTGCAAAAAAACTAAATCAAAAAAAAAAGAACAAGAACATGGGGAAGGG 2373 2236 ACTCAGTCCTGAAAAAAAATCAACAAGAAAAAGAGGTAAGGCGAACTGGG 2295 2374 AGGTCCTCAATCTGACCAAGGGTTTCCAAGGGTAAGCGGTCTCAGGC 2433	2494 AGGCGGTGTGCGGGGTGCTGCGGAGGAGCCCCGGCTGTCTTCGCAAATCCT 2553 2416 AAGCAGTAGACAATGAACCACCTGATTACAAGAGCCTCATTCCTCTGGAACGTCAGTCA
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	AGAAGCTAATTGATCAAGAAATCAAGTCTCAGGAGGAGGAGGAGGAAAAAAGAGAAAAAAGGCCACAAGAAAAGGGAGAAAAAGGCCAAGAAAAGGTCAAGAAGAGGAGAAAAAGGTCAAGACCTTGGCCCTCATGTTGGTGGGGGGGG	99 CCACAAATGCAAAGCATACCAAACTAGCCCTTGCTGAAGCCAGAGTTCAGGAGG 858 946 ACCGCCAGAAGCTGCAAGTTAGAAGTGGACTTCGAAGGCTTCAGGAGG 858 946 ACCGCCAGAAGCTGCAAGTTGGAACTTCGAAAGGCTTCTCCC 1005	979 AACAAAAGCTGGCAGCACGCAGCAGATTGATGAGAGAGAG		1279   TTATGGCTCTGGAAAAGTTAGAAAGCGTTTCAACAAAAGCAACAAGAATGCTACTCTC   1338     1426   TCATCTGAACCTCGAGAAGGAAAGCAACTAACCAAAGACGAGCTGGTGAAGG   1485     1339   TGAAATGCAATTTAGAAAAAGAAACGATGCTCCAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAAGCATGTCTCCAAGAACTGAAGAATGCAATTTAGAAAAAGAACGATGACTCCAAAGAAGAATGCTCAAGAACTGAAGATGCTCAAGAAGAAGAATGCTCAAGAAGAAAGA

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The present full-length cDNA sequence encodes GIP90, a novel 90 kDa

Goodpasture antigen binding protein (GPBP) interacting protein. The cDNA

Goodpasture antigen binding protein (GPBP) interacting protein. The cDNA

was isolated following a yeast two-hybrid screen for GPBP interactive

proteins and use of a partial clone to screen a human skeletal muscle

CC proteins and use of a postial close to chromosome 3 (3412).

CC mach library. The GIP90 gene was localised to chromosome 3 (3412).

CC madenine at position 2720 in the cDNA that was not present in GIP90

CC mocded a 130 kDa protein (GIPJ03a) and resulted (see ACC8322B) that

CC encoded a 130 kDa protein (GIPJ03a) and resulted from faithful

CC mocded a 130 kDa protein (GIPJ03a) and resulted sequence (i.e. no

A2720. GIP90/130 polypeptides interact with GPBP and are capable of

A2720. GIP90/130 polypeptides interact with GPBP and are capable of

CC aggregation. They can be used to modify GPBP-GIP90/130 interactions, to

modify GP90/130 aggregation, and to modify GPBP-GIP90/130 polypeptides, portions of them, antibodies,

concleic acid sequences, expression vectors and host cells, as well as

CC methods for treating an autoimmune disease or cancer by modifying the

CC expression or activity of one or more GIP90/130 polypeptides
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                                                                                                      New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or
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Best Local Similarity 55.2%; Pred. No. 8.7e-172;
Matches 1679; Conservative 0; Mismatches 1329;
                                                                                                                                                                                                Claim 48; Page 54-59; 115pp; English.
                                Revert-Ros F;
(REVE/) REVERT-ROS F.
                                                                 WPI; 2003-505281/47.
P-PSDB; ABR62250.
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                                                                                                                                                                                      2767 chhirtenacacadagaereercherrhacacadhacrecadrahacadhacherd
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473. .2767
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20-MAY-2002;
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14.3   GGGTCACCACCCGAAAGAGGACCTGACCGAAGCTCATTTGCTTTGCTTTGCTTTGCTTCAGGTCGACGTCGAAGACCCGAAGACCCGAAGCCGAACCCCGACCCCGAAGCCCGAAGCCCGAAGCCGAACCCCGCACCCCCTCCAAGCCGCCAAACCCCAAGCCGAAGCCGAACCCCACCCCTCCAAACCCGAACCCCAAACCCCAAACCCCAAACCCCCAAACCCCCAAACCCC	1606   GGANAAATTGATGGAGAAATAAAGCAAGAAGGGAAAGTGGATGGA
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2759 2612 2732 2403 CCATTGAGGATGACCTCATGAAAACAGAAGATGAATTATGAGACTCTAGAACGAAGGTATG 2462 2314 ATTCGGTCCTTCAGCAAAGATTTATGG-AAGAAGAACTAAGAACAAGAACATGGGGGAGG 2372 2432 2819 2492 2880 GAAGCAGTAGACAATGAACCACCTGATTACAAGAGCCTCATTCCTCTGGAACGTGCAGTC 2939 2672 3054 CTATGGATTCCCTGGATGAAATCCAAGGGGCCATCTTCAGAATGGAAAAATGCAA--- 3110 3170 CAGCCCCTACACATCCGTGTGACACCAGATCATGAGAACAGCACTGCCACCCTGGAGATC 2852 3171 CAGCCACTTCATATAAAGGTTACTCCAGACCATGTACAAAAACAACAGCCACTCTTGAAATC 3230 2853 ACAAGCCCCACATCTGAAG-----AGTTTTTCTCTAGTACCACCGTCATTCCTACCTTA 2906 2907 GGCAACCAGAAACCAATAACCATTATTCCATCACCAATGTCATGTCGCAAAAGCCC 2966 3291 GCCACGCCAAAGCAAAGGATAACCATCCTCCCAAAACGCCTCCATAACACCAGTAAAGTCC 3350 2343 AGATTAAGGAGCTCTCTCAAGAAGTGGAAAGACTGAAACTGAAGCTAAAGGACATGAAG 2402 TGGCCAAGCACAAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGAC 2193 2523 TIGCTAAGTACAAGTTAGCAGAAAAAAAGACC---AGCCATGAACAATGGCTTTTCA 2579 2580 AAAGGCTTCAAGAAGAAGCTAAGTCAGGGCACCTCTCAAGAGAAGTGGATGCATTAA 2639 2820 CCTAGTCTCAATGGAAGAAGTTTCCGATCCTCAAGTATTTTCTAAAGAAGTTCAGACA 2879 GAGGCGGTGTGCGGGGATGCTGCGGAGGAGGAGCCCCGGCTGTGTTCATTCGCAAATCC 2552 2940 Arcaargercagrrarargaggagagigagaarcaagaggaggaggaccraarga----r 2993 2994 gagggarichgregerectricaangerageeageraretrecargregergraagaaag 3053 2733 CCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGAGCTGGTCCTAGCACCAAAGCAGGGC 2792 2283 AAAACAAATTAAATCAAGACTCTGGGAAATCCACAAGACATTACACCAAGAAAACAATA 2342 2014 TGGTGGAGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCA 2073 GAACCGAGCAGGATAAGGCAAACTTCCTCCCCAGCAGCTCGAGGAAATCAAACACCAAA 2133 2463 CTAATGAACGAGACAAAGCTCAATTTTTATCTAAAGAGCTAGAACATGTTAAAATGGAAC 2522 2194 ACAGGTTTCGGCTGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCA 2253 AGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACT 2313 ACTCRGTCCTGCAAAAAAAAACTAAATCAAGAAAAACAGGAACAGTTTAGGAAGA ccaagradaaacagccaaagaaragragacaraccrararacacracacagagacc GAACGGTCCTCGGTCCTCGACAGGTATCCCCCCAGCGAATGAGCTCACCATGAGGAAG 3111 ACTABACCCABIGCCABCTTTGTGCABCCTGGAGATCTAGTCCTAGCCACACACACGCGG AGATCAGAGAACTAACGCTTGAAATCGAGAGTGAAGAAAACGGCTCCAGCAGTTGGAGG GAGGICCTCAATCIGACCAAGGAGCTAGAGCTTICCAAGCGCTACAGCCGAGCTCTCAGG GAGATTGAAAACCTCACTAAGGAGTTAGAGAGGTACCGGCATTTCAGTAAGAGCCTCAGG TTCCAGGAGGAAAATCACATCATGAGTAATCTTCGACAGGTAGGCCTGAAGAAACCCATG 2673 TCTTGGATTCCTTGGATGAGAAAAGAGAAAACGGTCCTTCCACTCCGCAGGAGAAGGG GAGGTAGGTCGTGCAAGGGGTCTGAGTTCACC 2134 2254 2640 2373 2760 2493 2553 2613 3231 1906 2700 2433 2793

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AAAA---GIGCAGAICCIACICICGGCCCAGAACGAGCCAIGICCCCIGICACGAITACI 3023
                    3351 AAAACCTCTACCGAAGACCTCATGAATTTAGAACAAGGCATGTCCCCAATTACCATGGCA 3410
                                           3024 ACTATTTCCAGAGAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCA 3083
                                                                3411 ACCTTTGCCAGAGCACAGACCCCAGAGTCTTGTGGGTTCTCTAACTCCAGAAAGGACAATG 3470
                                                                                       TCCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCCACTGAAATCGCTGTCTCT 3143
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                                                                                                                                                                             3204 ACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGAC 3263
                                                                                                                                                                                                   3591 TCATCATGGCAGTTTCAGCGTTCAAACAGCAATAGCTCAAGTGTGATAACTACTGAGGAT 3650
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AATAAAATCCACTTCACTTAGAAATCTACATTCACTTAGAAAGCTGCAAGCT 3692
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05-OCT-2001; 20010S-0329186P.
26-OCT-2001; 20010S-034984P.
26-OCT-2001; 20010S-0349165P.
02-NOV-2001; 20010S-034918F.
09-NOV-2001; 20010S-034918P.
16-NOV-2001; 20010S-034918P.
16-NOV-2001; 20010S-0335975P.
03-DEC-2001; 20010S-033698P.
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P-PSDB; ABR69651.
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The invention relates to an isolated polypeptide associated with cell growth, differentiation and death (GGDD). Also disclosed are the polymolecutides encoding the polypeptides. The polympeptides and polymolecutides according the polymolecutides and polymolecutides are useful in diagnosing, treating and preventing concert, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. apilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. apilepsy, Huntington's concert, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. apilepsy, Huntington's concert, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. placyies) and concert inflammatory (e.g. placyies) and concert inflammatory (e.g. placyies) and concert in attenting the expression of fragments are useful in screening compounds for effectiveness as an agonist or antagonist of the polypeptide, Microarrays consisting protein-protein interactions, drug-target interactions, and gene protein-protein interactions, drug-target interactions, and gene concerts and profiles. Sequences alven in monitoring or measuring protein-protein profiles. Sequences alven in records ACC90578-ACC90634 represent polynucleotides encoding CGDD proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human proteins associated with cell growth, differentiation, and death (GDD), useful for diagnosing, treating and preventing diseases conditions associated with the aberrant CGDD expression e.g. cancer, AIDS, or epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 gaaddaactgcaaacgcadaccacaadcaaadtricaccaadaccaaatrarggcaa
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Best Local Similarity 54.1%; Pred. No. 2.2e-137;
Matches 1436; Conservative 0; Mismatches 1187; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3053 BP; 1124 A; 668 C; 664 G; 597 T; 0 U; 0 Other;
                                                                                                                                                                                                                       5; Page 345-346; 350pp; English
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Oy 2339 GGAAGAAGA Db 1815 TCAACAAGA Qy 2399 AGAGCTTTC Db 1875 AGAGAGGTA	1935	2519	2579	2639	2699 2169	Qy 2759 CCCGGGGA             Db 2226 ACCTGGAGA	Qy 2819 AGATGATGA         Db 2286 AGACCATGT	2873	2933	2990	3050 2526	3110 2586	Qy 3170 AAGGACTAT        Db 2646 GCATGCGAT	Qy 3230 CAACTCCAA         Db 2706 CAGCAATAG	Qy 3290 TCAGTITAA         Db 2766 TCCTTACAT	RESULT 14 AAH06432 ID AAH06432 standard; XX
1271 CGAGGCCCAGTGCCGGGAGCTGAAGAAGCTCCAAGAGGAAGAACACCAGCAAGGA 1330	AGCGTTCAGCCGGGGTAAGTCGGGAATGCACCCACCTCTGAACCTGGGGAAAGGAGGAGAAAGCTTCAGCCTTCAACCTTGGAGAAAGGAGAAAGCAACCAGCTCCATCTGAACCTGGAGAAAGCAAACAAA	1451 GAACCTAACCAAAGACTGGAAGGTGGAGGTGGTCAAGAGTCGAGTTAAAGAACT 1510 	1511 CGAATGCTCCGAGAGTAGACTGGAGAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAA 1570 	1571 GCTGAAGTCCTTCACTGTGATGCTGGTGAGAAAAAATATGATGAGAAAAATAA 1630 	1631 GCAAGAAGAGAAGAGGATGGATGGGTTGAATAAAACTTTAAGGTGGAGCAGGGAAAAGT 1690 	1691 CATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCGAATCTGA 1750 	ANTIGAGAAAAGAGTACAGTCTGACAAAGGAGGGATGAGCTGATGAGTAAACTGAG	GAGCGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGATTACTAAAGAAGGGCT	1871 TGATGGCATAGAGGGGAAAAAAAACCGAGGTCGGCGCGCGC		1979 GGAGAGACTGAAGAAAGGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGGACTTGATGAAGAC 2038	2039 CGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACCGAGCAGGATAAGGCAAACTT 2098 1518 AGAAGATGAATATGAGAACGAAGGAATGCTAATGAACGAGAAAGGTCAAATT 1577	2099 CCTCTCCCAGCAGGAAAATCAAACACCAAAAGGCAAGGACAAAGCCATAGAGAA 2158 	AGGGGAGGCCGTGAGCCAGGAACTGCGACACAGGTTTCGGCTGGAGGAGCTTA	2219 AAGTCGTGATTTACAGGCCGAGGTGCAGGTCTCAAGGAAGATCCACGAGCTGATGAA 2278 1695 GTCAGGCCTCTCAAGAGAAGTGGATGCATTAAAAGAGAAAATTCATGAATACATGGC 1754	2279 CAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGATTTAT 2338 
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2518 CCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGT 2458 ACCCCGGCTGTGTTCATTCGCAAATCCTTCCAGGAGGAAAATCACATCATGAG 2578 BATCTAGTCCTAAGCCACACACCTGGGCAGCCACTTCATATAAAGGTTACTCC 2285 CTAGTACCACCGTCATTCCTACCTTAGGCAACCAGAAACCAAGAATAACCAT 2932 NATGCTAATATCATCACCACGGAAGACAATAAAATTCACATTCACCTGGGTTC 3289 GACAGGTAGGCCTGAAGAACCCATGGAACGGTCCTCGGTCCTCGACAGGTA 2638 CTACTCCATGTCCTGTTAACAGAAAGCTATGGATTCCCTGGATGAAATCCAA 2168 zatettergaatggaaaatgeaa---aetaaaeeeaatgeeaaetttgtgea 2225 SAGCTGGTCCTAGCACCAAAGCAGGCCAGCCCCTACACATCCGTGTGACACC 2818 AGAACAGCACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAG-----A 2872 CACCCAATGTCATGTCGCAAAAGCCCAAAA---GTGCAGATCCTACTCTCGG 2989 ACGCCTCCATAACACCAGTAAAGTCCAAAAACCTCTACCGAAGACCTCATGAA 2465 sérrerenaciceadaaddacaarciceeraireageirriggereigae 2585 CAGCTCCCACTGAAATCGCTGTCTCTCAAATCTCAGGAAGTGCCTATGGG 3169 TCCTCAAAGTCACCCCGGAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTA 3229 raticadadrerecedadacegedagecareagedagetreagegetreaaa 2705 kaccrcarrecrergaacarcacearcarcardargereagrarararangaagad 2054 zakgacgaggaccraarga----rgaggarcrgrgcrgrccrrcaarg 2108 SCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAG 2698 GGAGCGCCTTTGCCGACAGGCCTGCATCCCCATCCAAATCATGACGGTGTC 3109 craccrercies de accente centre de la constante del constante de la constante de la constante de la constante del constante de la constante de la constante de la constante de la constante del constante del constante del constante del constante de la constante del constan CTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGA SGTCCTTCCACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCA BAAACTAAGAACAAGAACATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCT CDNA; 844 BP. AGCGATCT 3305 TGCAAGCT 2781

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2259 AAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCG 2318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2499 GTGTGCGGGGATGCTGCGGAGGAGGAGCCCCGGCTGTGTTCATTCGCAAATCCTTCCAG 2558
                                                                                                                                                                                                                                                                                                                                                                                                541 AAGATTCACGAATTAATGAACAAAGAAGATCAGCTTTCTCAGCTCCAGGTAGATTATTCT 600
                      1959 AGAGAACTAAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTG
                                                                                                                                                                                   241 AAGGAACTAACACTTGAAATTGAGAGACTGAAGAAACGTCTCCAACAATTGGAAGTGGTC
                                                                                                                                                                                                                     2019 GAGGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACC
                                                                                                                                                                                                                                                      301 GAAGGGGATTTGATGAAGACAGAAGATGAGTATGATCAGCTGGAACAGAAATTTAGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, nootropic, immunosuppressant, cytostatic, gene therapy, cancer, peripheral nervous system; neuropathy, central nervous system; CNS; Alzheimer, sp. Parkinson's disease; Huntington's disease; haemostatic, amyotrophic lateral sclerosis, SNy-Drager Syndrome; chemocactic, chemotinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                           ATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATC
                                                                                                                                                                                                                                                                                                                                                                   2139 AAGCACAAAGCCATAGAGAAAAGGGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                          2199 TTTCGCTTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 TTTCGGTTGGAAGCTAAAAGTCGGACTTAAAAGCCGAAGTACAAGCTCTTAAAAGAG
                                                                                                                                                                                                                                                                                            2079 GAGCAGGATAAGGCAAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAACACCAAATGGCC
                                                                                                                                                                                                                                                                                                                   23.79 CTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGGAGCTCTCAGGCCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 CTCAATCTGACCAAAGAGTTGGAGCTTTCCAAGCGCTACAGGCAGAGCTCTTA-GCCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2439 GGGAACGGCCGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGGGTGCAGACCGAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               720 GIGAAIGGAAGAAIGGIGGAIGIICCIGIGACGICAACIGGAGICCAAACIGAIGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 4947.
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length cDMAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand or a polymucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the functional comprises at least 15 mucleotides, or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the polymucleotide comprises a 1'-end sequence; where the coligonucleotide comprises a 1'-end sequence; where the coligonucleotide comprises a 1'-end sequence; where the coligonucleotide comprises at least 15 nucleotides and the compination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are least 15 nucleotides and the compination of particularly full-length cDNAs. The primers are also useful for the selection and/or dagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the clear companion of the full-length cDNAs. The primers are also useful for AAH13628 and AAH13632 to AAH13634 to PAB95893 represent human amino acid sequences; and AAH13639 to AAH13632 represent contraction of the collaboration of the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAAGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACA 1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
cDNAs.
                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1779 AAGGAGGATGAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAGGTCCTGTGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ery Match 13.3%; Score 581.6; DB 4; Length 844;
st Local Similarity 81.1%; Pred. No. 4.4e-126;
tches 685; Conservative 0; Mismatches 159; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 3267; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Isogai T, Nishikawa T, Hayashi K, Saito K, Y. Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                       Human cDNA clone (5'-primer) SEQ ID NO:3267.
                                                                                                                                                                                                                                                                                                        27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-0018776.
02-MRY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                    28-JUL-2000; 2000EP-00116126
                                   26-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                        29-JUL-1999;
                                                                                                                                            Homo sapiens.
                                                                                                                                                                               EP1074617-A2.
                                                                                                                                                                                                                07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunouppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous sinjuries, peripheral nervous injuries, call diseases, such as localised neuropathies and central nervous system disease, amyotrophic localised neuropathies and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, activity, chemotexcic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGACAACAGGTGGGAATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCAAAAAAGAAGAAGAAATCAAATAGGAAGGAGGATGATGGTCATGGCCTCAGGAACTGT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACTGGGTTCTTCAAAGGATAAACTACCTACATAGAGGACATACCTTTGGTTAAAGGAG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCCGTCAGGTGGGAATGAGATCTCGAAACCAAGGTGGTGAAAGTGCATCTGATGGGCA 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATCTCCTGTCCCAAGCCCTCCATCATCGGCAATGCTGGTGAAAAAAGTCTCTCAGAAGA 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCAAAAAAGAACAAG---GCCAATCGGAAGGAGGAGGATGTCATGGCTTCCGGAACTAT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAAAGGCACCTCAAACCATCTGGAGAAAGTGAGAAAAAGACTAAAGAAGTCTGTGGAGTT 295
                                                                                                                                                                                                                                                                 Wang D;
J, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAACGACACCTAAAAACATCTGGAGAATGTGAACGAAAAACTAAGAAATCCCTGGAGTT 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCCAAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGA 355
                                                                                                                                                                                                                                                                                                                                                                             Buch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACTGGGTTCTTCAAGGGATAAACCAGCGGC-GAAAGAACACACCATTGGTT-AAGGAG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders
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Zhang J
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                                                                                                                                                                                                                                                                 Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 13.1%; Score 570.2; DB 4; Local Similarity 86.5%; Pred. No. 2.6e-123; Ne 664; Conservative 0; Mismatches 99;
                                                                                                                                                                                                                                                                 Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 4947; 10078pp; English.
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hrman T, Xu C, M
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                          central nervous system injuries.
                                                                                                                  20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00633036.
29-NOV-2000; 2000US-00727344.
                                                                       990S-00471275.
2000US-00488725.
2000US-00553117.
2000US-00598042.
2000US-00620312.
                                                                                                                                                                                                                                                             Asundi V,
Wehrman T,
                                           26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                             Liu C, Aeur
Wang Z, Wehr
Goodrich R,
                                                                                                                                                                                                                                                                                                                           WPI; 2001-442253/47.
P-PSDB; AAM41802.
                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
              26-JUL-2001.
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Wang J,
Zhou P,
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858 ATCCAAAGAAGACCTCATCCAACTACTCAGTATAATGGAAGGGGAGTTGCAGGCCAGAGA
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                                                                356 AGATGTCATCCACATGCTGAGGACAGAGAAAGCGAAGCCGGAGGTTCTGGAGGCACACTA
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Search completed: September 7, 2004, 23:08:55 Job time: 2370 secs

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TYPE: DNA ORGANISM: Homo sapiens
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Sequence 1065, Ap
Sequence 180, App
Sequence 137, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1126, Appl
Sequence 1126, Appl
Sequence 1126, Appl
                                                                                                                                                                                 September 8, 2004, 06:32:00 ; Search time 3716 Seconds (without alignments) 5837.425 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 6
Sequence 4
Sequence 2
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| Ggn2_6/ptodata1/1/pubpna/US07_NEW_PUB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US06_NEW_PUB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US06_PUBCOMB.seq:*
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| Ggn2_6/ptodata1/1/pubpna/US07_NEW_PUB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US08_PUBCOMB.seq:*
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| Ggn2_6/ptodata1/1/pubpna/US09_NEW_PUB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US09_NEW_PUB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US09_NEW_PUB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US10B_PUBCOMB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US10B_PUBCOMB.seq:*
| Ggn2_6/ptodata1/1/pubpna/US10_NEW_PUB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-10-117-722-1065
US-10-116-802-1065
US-10-108-260A-1637
US-10-309-851-15
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US-10-309-851-11
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US-10-071-766-132
US-09-960-706-972
US-09-873-319-634
US-10-171-311-47
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## ALIGNMENTS

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US-10-037-270-1065

j. Sequence 1065, Application US/10037270

j. Baginere 1065, Application US/10037270

j. Baptication No. US20030104529A1

j. GENERAL INFORMATION:

j. APPLICANT: Tain, Chenghua

j. APPLICANT: Asundi, Vinod

j. APPLICANT: Chen, Rui-hong

j. APPLICANT: Chen, Rui-hong

j. APPLICANT: Chen, Rui-hong

j. APPLICANT: Chen, Rui-hong

j. APPLICANT: Asundy, Jian

j. APPLICANT: Wenkman, Yonghong

j. APPLICANT: Wenkman, Yonghong

j. APPLICANT: Wang, Yonghong

j. APPLICANT: Wang, Jian-Rui

j. APPLICANT: Where I John

j. APPLICANT: Wang, Jian-Rui

j. APPLICANT: Wa
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 us-10-788-793-1.rnpb

AGGAGCACCAGCTGAGATTGCAGTTTTCTCCCGAATCCCAGGAAATGCCCATGGGACGGAC	4134 AAAAATATTTGAAATAGGACAGAGTTTAACACTTGTCATTTTGCACTATCAAGCCATGA 4193 4679 AATCCTATTACAAAATAAGACATACTTTAACTATTGCATTTTGCACTATCACATGA 4738 4194 GTTTGATATAAGAGATAAAAAAAAAAAAAAAAAAAAAA
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	3056 AAGGAGCGCTTTGCCGACAGGCCTGCATCCCAATCATGACGGTGTCAACATC 3115

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FIGARTCTGCAGAACCTGAGAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCA  GGGTCTGCAGAACCTGAGAAGTGCTTCGGGTCCTGCACCGAGATGCCATTCTTGCCCA  GGGTCTGCCGGAGCCAGAGAAGTGCTTCGGGTCCTGCACCGAGATGCCATTCTTGCCCA  GGGAAAACCCCATAGGAGAAGTTCTATGAGAAACCCATTCTCAGAGCTGGACAGACTGA  GGGAAAACCACAGGAGAAGATGCTTATGAGAAACCCATTCTCAGAGCTGGACAGACTTGA  GGAAAAACACAGAAGAAGATGCTATGAGAAACCGATTTCAGAGCTGGACAGACTTGA  GGAAAAACAGAAAACAGAACACCTGCCCGCATGCTAGAGCAGCTGTTGCTGGTGGACAGATTGA  GGAAAAACAGAAAACGAACACCTGCCGCATGCTAGAGCAGCTGTTGCTGGTGGAGAAGTG  TCATAGGCGCCCCCTTATCACCAACCTGCTAGAGCAGCTGTTGCTGGTGGTGAAAGTG  TCATAGGCGACCTTCACCAACCTGCTGGAGAAGCACTAACACTGAAAGAATGAAACACTTCACCAACCTGCTGGCTG	1578   AGAGATGATGATGATGAGAGTCTCACAATAGGCAACTTAGACTCAAGCT   1637   1638   AGAGATGATGAGCGTAATCAGAGAGTCTCACAATAGACTCATGAGAGTCTCACATAAACTCAGAGAGTCTGAAAGAGTCTCAGAAGAGTCTCAGAAGAGTCTAACCCAAAGAGTCTGAGAGAGTCTGAAAATCTGCAGAAGAGCT   1638   GGTTGGCTTAACCCAAAGAGTCTAGAGAACTCTCAG   195   116   AGAGGAAGAACTCCAGGAGATAAAATTGCCAAAGGAGAATGTGGAAACTCTAG   1757   116   ACAGGAAGAACTCAAGAAATTAAGAGATAAAATTGAAAGAGATGAAGAGAAGA
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	3438 TTTTCTAGTACCACTGTCATTCCTACCTTAGGGAATCGGAAACCAAGAATAACCATTAT 3497 2936 TCCATCACCCAATGTCATTCCCAAAAGCCCAAAAGTCCAGATCCTACTCTCGGCCCAGA 2995 3498 TCCATCACCAAACGTTATGCTCAAAAAACAAAAAGTGGAGATACTACTTTGGCCCAGA 3557 2996 ACGAGCCATGTCCCCTGTCACGATTACTACTATTCCAGAGATACTACTTTTGGCCCGGAAGGTGG 3055 3558 ACGAGCCATGTCCCCAGTCACAATACTACTACTTTTCCAGAGAGAAGAGGG 3617 3558 ACGAGCCATGTCCCCAGTCACAATTACTACATTTTCCAGAGAGAAGAGACGAAGATGG 3617 3056 AAGGAGCGCTTTGCCGACAGCCTGCATCCCCATCCCAAATCATGAGAGAAGACTCCAGAAAGTGG 3617 3056 AAGGAGCGCCTTGCCGACAGCCTGCATCCCCATCCCAAATCATGAGACACACTCTACAACTC 3115 3115	TGCAGCTCCCACTGAAATGGCCCCCCTATITAAATTGCGAAGGACGAAGGACCATGGGAAGGACCATGGGAAGGACCATGGGAAGGACCATGGGAAGGACCATGGGAAGGACCATGGGAAGGACCATGGAAGACTGCTCCCAGGAAATTCCAGGAAATTCACATTCCAGTAATTCACATTCCAGTAAGGAAGAATTCACATTCCAGTAAGGAAATTCACATTCACTTCAGGAAATTCACATTCACTTCAGGTTCTCAGTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCTCAGTTCACTTC	TAAGGATCTCCTGGCCTGCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGT	AACGTCATCCACCACGAGGAACCCAATCAGGACAAGATGGGTCATCTCAGCGGCCCAACGTCATCCACGGGGCCCATCAGGGACAAGACGTCAAGACGTCAAGACGTCATCTCAGGGGCCCTATCTGCTGGGGACAAGACGGCTCATCTGCTGGGGACCAAGACGGCTCATCTGCTATGTCAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGCCTATGTCCAATGTCCAAAGGTATGAAAGCTGGAAAAGCCAGAAATCCAACTGTATCCAATGTCCAAAATCTGAACAAATCCAAGAAATCTGAACAAATTCGAGCCTGAGGAAAATTCGAGCCTGAGGAAAATTCGAGCCTGAGGAAAATTCGAGCCTGAGAAATTCGAGCCTGAGAAATTCGAGCCTGAGAAATTCGAGCCTGAGAAATTCGAGCCTGAGAGTTGAGAAATTCGAGCCTCTTGAGAGCTGAGAAATTCGAGCCTCTTGAGAGCTGAGAAATTCGAGCCTCCTTGAGAGCTGAGAAATTCGAGCCTCCTTGAGAGCTGAGAAATTCGAGCCTCCTTGAGAGCTGAGAAATTCGAGCCTCCTTGAGAGCTGAGAAATTCGAGCCTCCTTTGAGAGCTGAGAAATTCGAGCCTCCTTTGAGAGCTGAGAAATTCGAGCCTCCTTTGAGAGCTTGAGAAATTCGAGCCTCCTTTGAGAGCTTGAGAAATTCGAGCTTGAGAAATTCGAGCCTCCTTTGAGGGGGGAAGCTGAAAATTCGAGCTCTTTGAAGAGCTGAAAATTCGAGCTTGAGAGCTTGAGAAATTCGAGCTTGAGAGCTTTGAAGCTGAGAAATTCGAGCTTGAAAATTCGAGCGCAGCAGCAGCACTCTTTGAAGAGCTGAAAATTCGAGCTTTGAAGAGCTGAAAATTCGAGCTTGAAAATTCGAGCGAG
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Publication No. US20040005560A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SEQ ID NO 1637
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Pred. No. 2.1e-311;
0; Mismatches 238; Indels
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US-10-108-260A-1637
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                  AATCGCTGTCTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCAC
                                                                         CCCGGAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCAT
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: GIP130b
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    NAME/KEY: CDS
    LOCATION: (12)..(3410)
    OTHER INFORMATION:
    US-10-309-851-13
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                                                                                                                                  TCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAA 655
                                                                                  TCATAGGCGCACCGTATACGAGTTAGAGAACGAGAAGCATAAACACACTGACTACATGAA 846
                                                                                                                CAAGAGCGACGACTTCACCAACCTGCTGGAGCAGGAGGAGGAGGAGGATGAAAAAGCTCCT 715
                                                                                                                                                                          TGAACAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAAAGGCTAAGCGGCTCAACAA 775
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727 GGAAAAACGAAAAGAAACCTACCGGCGCATGCTAGAGCAGCTGGTGGTGGTG
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Sequence 13, Application US/10309851
Publication No. US20030108554A1
GENERAL INFORMATION:
APPLICANT: Saus, Juan
APPLICANT: Revert-Kos, Francisco
TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REPRENCE: 98, 722-F-05
CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT APPLICATION NUMBER: US/10/309,851
SOFTWARE: Patentin version 3.1
SECTION OF SECTION 9 345 202 cagaadacerereaagadardacererrarrererereagearreredadoaaaaerde 261 346 AGGCTCGAGAAGATGTCATCCACATGCTGAGGACAGAAAACCAAGCCCGAGGTTCTGG 405 262 AGGCTCGAGATGAGGTCATAGGCATTTTAAAGGCTGAAAAATGGACCTGGCTTTGCTGG 406 AGGCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCA 465 322 Aagereagrareserriereaereesaaaaasererreesaseserereesasasaassa 381 466 TCCTTGCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGG 525 441 526 ACAGACTGGAGGAAAAGCAGAAGGAGACGTACCGCGCATGCTAGAGCAGCTGCTGCTGCTGG 585 442 ACAAAGTTGTGGAAAAAAAAAAAATCTTACAGACGAATCCTGGGACAGCTTTTAGTGG 501 586 CTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACTG 645 502 cadaaaaarcccaracccaraccararredacriddadgaadaaaaaaaaacaraaag 561 705 AAAAGCTCCTTGAACAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAAGGAAAACGCTAAGC 765 825 826 ACGAGAGGCAGATGCACATCGAGCAACTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCA 885 886 CTCAGAAGCTGAGGGAGGAGGAAGAAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAG 945 682 GGGTCACCACCCTGAAAGAAGGAGCTGACCAAGCTGAAGTCTTTTGCTTTTGATGGTGGTGG 742 ATGAACAGCAAAGGCTGACGCCACAGCTCACCCTTCAAAGACAGAAAATCCAAGAGCTGA 801 286 CTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGGGAGTTGC 646 ACTACATGAACAAGAGGGACGACTTCACCAACCTGCTGGAGCAGGAGCGAGGGTTGA 766 GGCTCAACAAACTTCGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGG Query Match
Best Local Similarity 55.2%; Pred. No. 1.7e-202,
Matches 1680; Conservative 0; Mismatches 1388; Indels 33;

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AGATTAAGGAGCTCTCTCAAGAAGTGGAAAGATATGACCAGTTAAAGGACATGAAAG TGGTGGAGGGAGTTGATGAAGACCGAGGAGATATGACCAGTTAGAGGATTGA CCATTGAGGATGACTCTCCCAGGAGCTCGAGACTCCAAGACCCAA CCATTGAGGATGACTCCATGAAAACGAGAGTGAACTTCTCCAAGACCCAAA CTAATGAACGACAAAACCTCAATTTTTATTTTA	2614 AACGGTCCTCGGTCCTCGACAGGTATCCCCCAGCGGAATGAGCTCACCATGAGGAAGG 2673  [
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646 ACTACATGAACAAGAGCGACGACTTCACCAACCTGCTGGAGCAGGGGGGGG	706 AAAAGCTCCTTGAACAAAAAAGCTTACCAAGCCGGCAAAAAAAGGAAAACGCTAAGC 765 	766 GGCTCAACAAACTTCGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGG 825	826 ACGAGAGGCAGATGCACATCGAGCAACTGGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCA 885 	886 CTCAGAAGCTGAGGGAGGAAGAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAG 945	946 ACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTTCGAACACACAGGCCTCGAGGTTTTCC 1005	1006 AGGAGCACGAAGAGATGAACGCCAATTGGGGAATCAAGAATCTCACAACCGGCAACTTC 1065	1066 GACTCAAACTGGTTGGCAAAGGATTGAGGAGGTGGAAGAGACCAATAAAAGCC 1125 	1126 TTCAGAAGGCAGAGGAGAGCTCCAGGAGCTGAGAGAAAATTGCCAAAGGGAATGTG 1185 	1186 GAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGCGTGCTTGAGATGGAGG 1245	1246 GCAAGGATGAAQAGATCACGAAGACCGAGGCCCAGTGCCGGGACTGAAGAAGAAGCTCC 1305 	1306 AAGAGGAAGAACCCACAGCAAGGAACTTAGACTAGAAGTGGAGAAGCTGCAGAAGAGGA 1365 	1366 TGTCTGAGCAGGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGC 1425	1426 TCCATCTGAACCTGGAGAAGGAGAACCTAACCAAGACCTGCTGAACGAGCTGGAGG 1485	1486 TGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGT 1545 1399 GTTTAAAAGTAAGGATCAAAGAGCTAGAAGCCATTGAAAGTCGGCTAGAAAAGACAGAAT 1458	1546 TAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCGTGGATGAGA 1605 1459 TCACTCTAAAAGAGGATTTAACTAAACTGAAAACATTAACTGTGATGTAGTTTGTAGAGATGAAC 1518	1606 GGAAAAATATGATGGAGAAAATAAAGCAAGAAGAGAAGGAAAGTGGATGGA	1666 ACTTTAAGGTGGAGGAAAAGTCATGGATGAGGGAAAGCTAATCGAGGAAAGCA 1725
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QY         3085         CCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTGAAATGGCTGTCTCT         3144           Db         3010         CCCTAATTCAGGTTTTGGCTGAATTCAGTTCAGCTAGCTCCTCGAGCAGGAGCGCTCCT         3069	3145 CTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCGGAAAAAAAA	3130 CHGTTCCAGCCCCGGAGAAGAACAACAACAATGTAAATATCATCACGCAGGAAGACA	3265 ATAAAATTCACATCACCTGGGTTCTCAGTTTAAGCGATCT 3305 3160 ATAAAATTCACATTCACATCAGTTTAAGCGATCT 3305 3100 ATAAAATTCACATATCATTAAACAATCATCT 3305	9 I/IS		APPLICANT: Saus, Juan ; APPLICANT: Revert-Ros, Francisco ; TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity ; TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein	SATION NUMBER: S DATE: 2002- ID NOS: 38		; OKGANISM: Homo sapiens ; FEATURE: ; OTHER INFORMATION: GIP130C	; FAILURE: DS ; I.OCATION: (9)(3407) ; OTHER INFORMATION: US-10-309-851-15	Query Match Best Local Similarity 55.2%; Pred. No. 4.7e-202; Matches 1679; Conservative 0: Mismatches 1379; Indels 33; Gans 6:	286 CTGTGGAGTTATCCAAGAGGGCCTCATCCAGCTCCTGAGTATCATGAAGGGGGGGTGC 34	AGGCTCGAGAAGATGTCACATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGG	406 AGGCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCA 	466 TCCTTGCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGG 379 TTCAAGCAAATTACCCCTTGGCAGAAGAGACATCTATGAGAAACCAATGAATG	526 ACAGACTGGAGGAAAAGCAGAAGGAGAGGTACCGCCGCATGCTAGAGCAGCTGCTGG	586 CTGAGAAGTGTCACAGGGGCACCGTGTACGAGCTGGAGAAGCAGAAGCACAGGTGTGCACTG

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APPLICANT: Saus, Juan
APPLICANT: Saus, Juan
APPLICANT: Revert-Ros, Francisco
TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFRENCE: 98,723-F-US
CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
SOFTWARE: Patentin version 3.1
SEQ ID NO: 11
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                                                                         CAAGCCCCACATCTGAAG-----AGTTTTTCTCTAGTACCACCGTCATTCCTAGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 11, Application US/10309851; Publication No. US20030108554A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
OTHER INFORMATION: GIP130a
FEATURE:
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Best Local Similarity 55.2'
Matches 1679; Conservative
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; OTHER INFORMATION:
US-10-309-851-11
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Pred. No. 5e-199;
                                                                                                                                     0; Mismatches 1329;
                                                                                                   17.8%;
55.2%;
                                                                                                                    Best Local Similarity 55.2
Matches 1679; Conservative
   OTHER INFORMATION:
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GIP90
                                     ; NAME/KEY: mi
; OTHER INFORM
US-10-309-851-9
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APPLICANT: Saus, Juan
APPLICANT: Saus, Juan
APPLICANT: Severt-Ros, Francisco
APPLICANT: Revert-Ros, Francisco
TITLE OF INVENTION: G1Ps, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFERENCE: 98,723-F-US
CURRENT PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO9 SEQ ID NOS: 38
LENGTH: 3998
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Publication No. US20030108554A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (473)..(2767)
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US-10-309-851-9
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                                                                                                                                                                                Gaps
                                                                                                                                                                                33;
                                                                                                                                                          DB 16; Length 3069;
1.8e-141;
        APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1126
LENGTH: 3069
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                                                                                                                                                          12.9%; Score 565; 54.2%; Pred. No. 1
                                                                                                                                                                               Conservative
                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1126
                                                                                                                                                                    Similarity
GENERAL INFORMATION:
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Matches 1297;
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                  2127 garacceaacreredecacecaaaccaaaccaraaccarecerecaaaaccecerecaraac
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; OTHER INFORMATION: Incyte ID No. US20020192678A1 246064.2
US-10-071-766-12
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; Publication No. US200201926781
; GENERAL INFORMATION:
APPLICANT: Huel-Mei Chen
; TITLE OF INFORTATION: GENES EXPRESSED IN SENESCENCE
; TURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT APPLICATION NUMBER: 120/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SSOTWARE: PERL PROGRAM
; SEQ ID NO 132
; LENGTH: 3587
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 CACCCTGGAGATCACAAGCCCCACATCTGAAG--
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Sequence 972, Application US/09960706

Publication No. US2003013428041

GENERAL INFORMATION:

APPLICANT: Munger, William E.

TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplass

TITLE OF INVENTION: Gene Expression Profiles

TITLE OF INVENTION: Gene Expression Profiles

FILE REFERENCE: 4921-5029-01US

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/223,323

PRIOR APPLICATION NUMBER: 09/873,319

PRIOR PILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 1124

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 972

LENGTH: 3025
2455 GTCTTGTGGTTCTCTAACTCCAGAAAGGACAATGTCCCCTATTCAGGTTTTGGCTGTGAC 2514
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Pred. No. 3.9e-135;
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Best Local Similarity 53.0%;
Matches 1393; Conservative
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                                                                                                               AAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGC
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Publication No. US20030134324A1
GENERAL INFORMATION:
APPLICANT: Munger, William E.
APPLICANT: Kulkarni, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Wamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: 14921-5029-03
CURRENT PAPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
BARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOFTWARE: PatentIn Ver. 2.1
CGGCAGTCATCATGCCAGTTTCAGCGTTCAAACAGCAATAGCTCAAGTGTGATAACTACT 2542
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                                                                                                                   ; OTHER INFORMATION: Genbank Accession No. US20030134324A1 U53445 US-09-873-319-634
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TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
FILE REFERENCE: WRI-035
FILE REFERENCE: WRI-035
FILE REFERENCE: WS-02-06-13
CURRENT FILING DATE: 2001-06-13
FRIOR APPLICATION NUMBER: US 60/298,155
FRIOR PILING DATE: 2001-06-13
FRIOR PLING DATE: 2001-06-13
FRIOR APPLICATION NUMBER: US 60/335,936
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RESULT 13 US-10-171-311-47

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781 TCTGGGAAATCCACAACAGCATTACACCAAGAAAACAATAAGATTAAGGAGCTCTCTAA 840
                                                                                                                                                           841 GAAGTGGAAAGTGAAACTGAAGCTAAAGGACATGAAAGCCATTGAGGATGACGTCATG
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11.4%; Score 496.6; DB 15; Length
Best Local Similarity 53.8%; Pred. No. 5.2e-123;
Matches 1174; Conservative 0; Mismatches 974; Indels
     FILE REFERENCE: 98,723-F-US
CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 23
LENGTH: 2355
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                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (1)..(2355)
; OTHER INFORMATION:
US-10-309-851-23
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                                                                            GTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAGGAAGTGCCT 3164
                                                                                                                                                         2029 GCCAAGCATGCGATATTCAGAGTCTCCCCAGACCGGCAGTCATCATGGCAGTTTCAGCGT 2088
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                                                                                                                                                                                                                                                         2089 TCAAACAGCAATAGCTCAAGTGTGATAACTACTGAGGATAATAAAATCCACATTCACTTA 2148
CCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCATCCCCCCAATCATGACG 3104
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APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER.
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER.
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER.
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER.
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PILLING DATE: 2000-01-5
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,61
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; LOCATION: 1, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253,

; LOCATION: 1254, 1255, 1256, 1257, 1258

; OTHER INFORMATION: n = A,T,C or G

US-09-814-353-19975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19975, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
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Scoring table:

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK017709

Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730485H21 product:hypothetical Tropomyosin/Glutamic acid-rich region containing protein, full
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004
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Score

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AV241894 AV241894 BU401987 603483217 BX736046 BX736046

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/noce="unnamed protein product; hypothetical
Tropomyon/Glutamic acid-rich region containing protein
(InterPro|IPR000533, PROSITE|PS50313, evidence: InterPro)
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32.4%;
Best Local Similarity 94.6%;
Matches 1474; Conservative 0
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Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs

Be (Dosses I to 2079)

Rature 420, 563-573 (2002)

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/strain="CSPEL6J"
/db_xref="MAXI-003010"
/db_xref="MAXI-003010"
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                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohaza, E., Watsahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I \hat{\kappa} II Team.
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Nature 409, 685-690 (2001)
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Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Çenter Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
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Homo sapiens, Similar to KIAA1275 protein, clone IMAGE:4616553,
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Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH CONSOrtium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AGGTTAAAAAAGCTCCTTGAACAAGAAAAGGCTTAATCAAGCCCCGCAAAGAAAAGAAAAT
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Location/Qualifiers
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Pred. No. 4.4e-93;
0; Mismatches 153;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue type="Lung"
/clone_lib="NIH MGC_77"
/lab_host="DH10B"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)

Direct Submission Strausberg, R.

REFERENCE AUTHORS TITLE

ACCESSION

RESULT 2 BC029425

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NIH-MGC http://mgc.nci.nih.gov/.
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421 GAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGAAATGGCCGAAGGATGGTG
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                                                                                                                                                61 GAGGACGAATACGACCAGTTGGAGCAGAAATTCAGAACCGAGCAGCAGATAAGGCAAATTTC
                                                                                                                                                                                2100 CTCTCCCAGCAGCACGAAAATCAAACACCAAATGGCCAAGCCAAAGCCATAGAGAAA
                                                                                                                                                                                                   2460 GACGIGCCIGIGGCCICCACIGGGGTGCAGACCGAGGCGGTGTGCGGGAATGCIGCGGAAG
                                                                               2040 GAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACCGAGCAGGATAAGGCAAACTTC
                                                                                                                                                                                                                                             2160 GGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAA
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DB 10; Length 826;
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Pred. No. 4.5e-84;
0; Mismatches 58;
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Mus musculus
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKU19472 3240 bp mRNA linear HTC 20-SEP-2003 Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631422005 product:DOC1 homolog [Homo sapiens], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunco, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                             2638 ATCCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGA 2693
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                                                                                                                                                                                                                                                       2578 GTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGT
                                                                                                                                                                                                                                                                                       601 GTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGT
  421 TGGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGAAATGGCCGAAGGATGG
                                                                                                     481 TGGACGTACCCGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGG
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                                                  2458 TGGACGTGCCTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGG
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Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                       Group phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3240)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mammalia; Eutheria;
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/dev stage="whore of the page resistant" |
/lab_host="bulbo (Ti phage resistant)" |
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/clone lib="NIH BMAP HDO" |
/site_2 Not I; The library was constructed according Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction ,ligated with EcoR I adaptor , digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TATTGAAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Itsue Procurement: Dr. Jāmes Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CON Electribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAR)
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91.8%; Pred. No. 3.2e-83;
iive 0; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                          'organism="Mus musculus"
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'clone="IMAGE:30612297"
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1. .716
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1742 CAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGAGAGGGATGAGCTGATGGG 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 TAAACTGAAAGGAAGAAGAAGAAAGAAAGACATGATCTTGTCAAAAGTTACTATATTGAA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1862 GAAGCGGCTTGA------TGGCATAGAGGAGGTAGAAAGGGAAATAAACCG 1906
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                                                                                  301 AACACAGGGTAAACTAGCCCTTGCTGAGGCCCAGAGCTCAGGAAGAAGAGAGAACAAC 360
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                                         GGAGGAAGAAAAACTCAAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTGCT 961
                                                                                                                                                                       CAGACTAGAAAAAGAACTGCAGACACAGACCACAGAGTTTCACCAAAAACCAAAAT
                                                                                                                                                                                                                                                            421 TATGGCGAAGCTCACCAATGAGGACAGTCAAAATCGCCAGCTCCGACAGAAGCTGGCAGC
                                                                                                                                                                                                                                                                                                             1082 CTTATCGCAAAGGATTGAGGAGCTGGAAGAGCCAATAAAAGCCTTCAGAAGGCAGAGGA
                                                                                                                                                                                                                                                                                                                                       481 ACTCAGTCGGCAAATTGATGAGTAAGAAGAGCCAACGACCATTTAAGAAAAGCCGAGGA
                                                                                                                                                                                                                                                                                                                                                                                               1142 AGAGCTCCAGGAGCTGAGAGAGAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCAT
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                                                                                                                              CAAGTTAGAAGTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAGAT
                                                                                                                                                                                                                     1022 GAACGCCAAATTGGCGAATCAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              541 AGAGCTGCAGGATATAAAAGACAAATAAACAAGGGAGAATATGGAAACTCTGGCATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 CATAAAATGGAGGAGCAGTGCAGAGACCTCAATAAGAGGCTAGAGAAGAGACAGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1382 GCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCCAGCTCCATCTGAACCTGGA
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/tissue type="skin"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
1. .3240
/note="DOC1 homolog [Homo sapiens] (SPTR|Q13597, evidence:
PASTY, 88.3%ID, 100%length, match=2299)"
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14.2%; Score 620.8; DB 11; Length 3240;
Best Local Similarity 54.0%; Pred. No. 2.5e-83;
Matches 1442; Conservative 0; Mismatches 1187; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |db_xref="FANTON DB:4631422005"
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|db_xref="mG1:1912759"
|db_xref="taxon:10090"
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/strain="C57BL/6J"
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618 bp mRNA linear EST 20-JAN-1999
EST220101 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
ROVBS89 3' end, mRNA sequence.
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2446 ACAGACCCCAGAGTCCTGTGGTTCTGTGACTCCAGAACGGACAATGTCACCTATTCAGGT 2505
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Sutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat
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Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
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/clone_lib="Normalized rat ovary, Bento Soares"
/note="Organ: ovary; Vector: pT7T3Pac; Site_l: B
Site_2: Not1"
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Unpublished (1998)
Unpublished (1998)
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/db_xref="ATCC (inhost):2031381"
/db_xref="taxon:10118"
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   AACGCTTGAAATCGAGAGACTGAAAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGGA
                                                                          CTCTCAAGAAGTGGAAAATCTGAAGCTGAAGCTAAAGGATATGAAGCCATTGAGGATGA
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="teaxon.10116"
/clone="nrdgl-00062-f8"
/tissue type="Dorsal Root Ganglia"
/clone_lib="nrdgl (10855)"
/note="Vector: pspor1; Site_1: Sall; Site_2: Not1; rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGAGGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAAC
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                                                                                                                                                                                                                                   Angen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00062 row: f column: 8.
Location/Qualifiers
1. 606
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13.9%; Score 606; DB 14; Length 606;
Best Local Similarity 100.0%; Pred. No. 7.3e-81;
Matches 606; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dorsal root ganglia"
                                                                                                      Rattus.
1 (bases 1 to 606)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
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                                   ORGANISM
                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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AU130457 AU2-2002 844 bp mRNA linear EST 01-AUG-2002 AU130457 NT2RP3 Homo sapiens cDNA clone NT2RP3000868 5', mRNA
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/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1838
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                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ tbases 1 to 84]. Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-396
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project, 5'- & Maical Science, University of Tokyo, and Helix Research Institute of Medical Science, University of Tokyo, and Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AAGGAACTAACACTTGAAATTGAGAGACTGAAGAAACGTCTCCAACAATTGGAAGTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP3000868"
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/db_xref="taxon:10116"
/clone='Ul-R-BJOP_aio-f-08-0-UI"
/dev_stage="adult"
/lab_host="adult"
/lab_host="U-R-BJOP"
/clone_lib='Ul-R-BJOP"
/clone_lib='Ul-R-BJOP"
/clone_lib='Ul-R-BJOP |
/clone='Vector: pT73D-Pac (Pharmacia) with a modified
polylinker: Site l: Not I; Site 2: Eco RI; The UI-R-BJOP
library is a subtracted library/derived from the UI-R-BJOP
library is a subtracted library derived from the UI-R-BJOP
UI-R-ABI, UI-R-ACI, UI-R-ABI, UI-R-ABI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, UI-R-AFI, and
UI-R-AGI libraries These libraries represent tissues from
rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
canal at 15.5 dpc, and ventricle at 18 dpc. AV
canal at 15.5 dpc, and ventricle at 18 dpc. AV
canal the Oilogo-Track. The library was constructed as
described by Bonaldo, Lennon and Soares, Genome Research
6: 791-806, 1996."
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                                                                                                                2139 AAGCACAAAGCCATAGAGAAAAGGGGAGGCCGTGAGCCAAGGCCGAACTGCGACACAGG 2198
                                                                                                                                                                                                                                                                  2199 TITCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAG 2258
                                                                                                                                                                                                                                                                                                                                                                                                                    2259 AAGAICCACGAGCIGAIGAACAAGGAAGACCAGCIGICICAGCICCAAGICGACIAIICG 2318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2379 CICAAICIGACCAAGGAGCIAGAGCTIICCAAGCGCIACAGCCGAGCICICAGGCCGAGI 2438
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361 GAGCAGGATAAGGCTAACTTCCTCTCAACAACTAGAGGAGATCAAGCACCAAATTGCC 420
                                                                                                                                                                   421 AAGAATAAAGCAATAGAGAAGGTGAGGTTGTGAGCCAGGAAGCTGAAACTGAGACACAGAGA 480
                                                                                                                                                                                                                                                                                                                                       481 TITCGGTIGGAAGAAGCTAAAAGTCGAGACTTAAAAGCCGAAGTACAAGCTCTTAAAGAG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 AAGATTCACGGAATTAATGAACAAAGAAGATCAGCTTTCTCAGCTCCAGGTAGATTATTCT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 GTACTICAACAAAGATTTAIGGAAGAAGAAAATAAGAACAAAAACAIGGGGCANGAGGIT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 CTCAATCTGACCAAAGAGTTGGAGCTTTCCAAGCGCTACAGGAGAGGTCTTA-GCCCAGT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       720 GTGAATGGAAGAATGGTGGATGTTCCTGTGACGTCAAACTGAAGTGGAAGTCCAAACTGATGCA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory for Computational Genomics
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/mol_type="mRNA"
/strain="Sprague-Dawley"
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BF562820
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COMMENT
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TITLE
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                                                                                                                          3747 CTACTGCTGCAGTGGAAACAACCTTCCTCTGTGCCAACCCTTTCCTTGTACTAATT 3806
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Sel bp. mRNA linear EST 12-JUN-2000
UL-R-BO1-apo-a-05-0-UI 3', mRNA sequence.
UL-R-BO1-apo-a-05-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                     123 TTTGTGCATCTGTTTCAATGCAGGGAATAGAATTAATTAGCAGAATTTCTGTTTGCTGA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 ACATATGCTCCCAAAGGCTGGCTCCCAATTTTCCTAATTGTAAGCCAACTTTAATAGACT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 TCAGAGCTATCACAGGGTCTCTAAAACTTTTGGAAAAACAAAAGCCCCTAATATGGACCTCA 542
                                                                                                                                                                      3 CGAGGGCTGCAGTGGAAACATCCTTCCTCTGTGCCAACCTTTCCTTGTACTACTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 CAGTICITITITITITITICCAAAAAAAAATAITITIGAAATAGGACAGAGTITIAACAG
                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 TIGICALTITIGCACTATCAAGCCATGAGTTTGATATAGGGTTATAAGAAAAGAATACTT
Query Match 13.2%; Score 576.2; DB 10; Length 583; Best Local Similarity 99.5%; Pred. No. 2.1e-76; Matches 578; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4287 GGAAACAATTTGAACATGAAATAAAATGGAAATGAACTGTG 4327
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 785)
Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Whittington, J., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mysk, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M., Creation of genome-wide protein expression libraries using random activation of gene expression

Mat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) mRNA linear EST 21-APR-2001
Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                             162 CAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 GAGCGACGACTTCACCAACCTGCTGGAGCAGGAGGGAGAGGTTGAAAAAGCTCCTTGA 43
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="athersps RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
                                                            342 ATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGA
                               ATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGA
                                                                                                                       GAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGA
                                                                                                                                                                   282 GAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGA
                                                                                                                                                                                                               CAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAACAA
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Pred. No. 3.3e-74;
0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115,
Tel: 216 431 9900
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RST32708 Atherays RAGE Library BG213104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG213104.1 GI:13734791
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ilarity 82.4%;
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/clone lib="UI-R-BO1"
/clone lib="UI-R-BO1"
/clone lib="UI-R-BO1"
/clone lib="UI-R-BO1"
/clone lib="UI-R-BO1"
/clone lib a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at actailed described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
IAG TISSUE-cropus-striatum
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                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                               University of lowa 1375 MEBRF, lowa City, IA 52242, USA Tel: 139 335 9565
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleoride that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A trail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
                                                                                       1 (bases 1 to 582)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Pred. No. 5.9e-76;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                        Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
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                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                        Chordata;
Rođentia;
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                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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Best Local Similarity 99.3
Matches 575; Conservative
  Rattus norvegicus
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Gaps

Normalization and subtraction: two approaches to facilitate gene

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The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the Not1 site
and the oligo-dT track served to verify it as a clone from the
normalized embryo at 13 dpc library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
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                                                                                        Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Fat: 319 335 9250
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Pred. No. 3.9e-74;
0; Mismatches 0; Indels 1
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Seg primer: M13 Forward
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/strain="Sprague-Dawley"
                     Genome Res. 6 (9), 791-806 (1996)
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                       GAAGACAGACAGAATTGCTCAAGTTAGAAGTGGACTTTGAACACAAGGCTTCGAGGTTT
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
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AMGNNUC:NRDG1-00033-F9-A nrdg1 (10855) Rattus norvegicus cDNA clone
nrdg1-00033-f9 5', mRNA sequence.
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Genome Research
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
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                                                                                                                                                                                                                                           Length 553;
and the oligo-dT track. The library was cc described by Bonaldo, Lennon and Soares, 6: 791-806, 1996. AG TISUBE-ventricle at 15 dpc TAG_LISUB-TRACTES TAG_LISE-TRACTES TAG_ESPG-GTGTC"
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100.0%; Pred. No. 6.3e-73;
tive 0; Mismatches 0;
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Fax: 319 318 8250

Fax: 319 318 9256

Fax: 319 318 9565

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The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized ventricle at 15 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)

Seg primer: M13 Forward
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UI-R-BJOp-aio-f-08-0-UI.81 UI-R-BJOp Rattus norvegicus cDNA clone
UI-R-BJOp-aio-f-08-0-UI 3', mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 553)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
         TGCCAACCCTTTCCTTGTACTACTAATTTAAGTTTTTAAATATCTTGTTTATAAAATAACC
                                       167 ATTTAATAGCCATGCACCCCCCCCTCCATTTTGTGCATTTCAATGGAATAGA
                                                                                                                        ATTTAATAGCCATGCCCCCCCTCCCATTTTGTGCATCTGTTTCAATGCAGGGAATAGA
                                                                                                                                                                                                                                                                         107 ATTAATTAGCAGAATTTCTGTTTGCTGAATGTTCTGTTGAAGATGTTGGTCCAGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJOp_aio-f-08-0-UI"
                                                                                                                                                                                                                                                                                                                                                  3959 TTACTTCTAGCATGTCGCCCCATTCAAGGTAG 3991
47 TTTACTTCTAGCATGTGGCCCCCATTCAAGGTAG 15

    .553
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
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AWS25176/c
LOCUS
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TITLE
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PUBMED
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4218

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Search completed: September 8, 2004, 10:58:32 Job time : 16005 secs

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7, 2004, 12:59:38; Search time 150 Seconds (without alignments) 2282.984 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                     sw model
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US-10-788-793-2 6082 Title: Perfect score: Sequence:

1 MRSRNQGGESSSNGHVSCPK.....KIELKKSAASSTASLGGGKG 1212 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp20018:\* geneseqp2004a:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	·	df			SUMMARIES	
	Score	Query	Length	DB		Description
	6082	100.0	1212	9	ABP97029	Abp97029 Rat L-FIL
7	5696.5	93.7	1213	4	AAM40016	
m	5696.5	93.7	1213	9	ABP97031	
4	4838	79.5	965	ø	ABP97030	Rat S.
D.	3051	50.2	653	4	AAB93085	
9	2586	42.5	551	4	AAB93244	Aab93244 Human pro
7	2452.5	40.3	1133	φ	ABR62252	Abr62252 GPBP-inte
8	2444.5	40.2	1133	9	ABR62253	Abr62253 GPBP-inte
σ	2444.5	40.2	1135	9	ABR62251	Abr62251 GPBP-inte
10	1926	31.7	893	9	ABR69651	Abr69651 Human CGD
11	1828	30.1	764	9	ABR62250	Abr62250 GPBP-inte
12	1675	27.5	785	9	ABR62257	Abr62257 GPBP-inte
13	1645.5	27.1		ß	AAU84329	Aau84329 Protein D
14	1645.5	.27.1		9	ABR92070	Abr92070 Human cer
15	1040.5	17.1	233	4	AAM41802	Aam41802 Human pol
16	929	15.3		4	AAB63771	Aab63771 Human pro
17	893	14.7		9	ABR64181	-
18	893	14.7	1076	7	ADC31075	Adc31075 Human nov
19	893	14.7	1087	9	ABG74689	Abg74689 Human CGD
20	780.5	12.8	439	ო	AAB58157	Aab58157 Lung canc
21	769.5		350	9	ABR62249	Abr62249 GPBP-inte
22	. 677	11.1	265	9	ABR62248	Abr62248 GPBP-inte
23	618.5		384	9	ABR62264	Abr62264 GPBP-inte
24	618.5	•	386	9	ABR62256	Abr62256 GPBP-inte
25	602	9.9	274	7	ADB65199	Adb65199 Human pro

AAB63826 4BR62263 4BR62263 AAA016359 AAA016359 AAA016359 AAA016359 AAAA78854 ABC20278 ABC20278 ABC20278 ABC30278	Aab63826 Human pro Abr62263 GPBP-inte Abr62247 GPBP-inte Aab63875 Human pro	Human Novel	Aam78854 Human pro Adb70370 PAC 6802 Add47946 Human Pro	Abg01716 Novel hum Aam40883 Human pol Abj10604 Human nov	Aam39097 Human pol Abr53116 Protein 8 Aam79838 Human pro	Abp73809 Candida a Abg065505 Novel hum Aau84350 Protein M Abr92127 Human cer
	AAB63826 . ABR62263 ABR62247 AAB63875	AAO16359 ABG20279 ABG20278	AAM78854 ADB70370 ADD47946	ABG01716 AAM40883 ABJ10604	4AM39097 4BR53116 4AM79838	<b>АВР73809</b> <b>АВСО6505</b> <b>ААU84350</b> <b>АВК92127</b>
	4004	044	4 ~ ~	440	404	24 4 0 4
40040444CC44CG4C4C	190 240 240 225	2349 2415 2400	1960 1960 1960	2143 2688 1959	2663 1790 1963	1881 2633 1857 1938
2440 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4.08 4.0.08 4.0.08	7.8	7.7	r.r r.r	7.7	7.6 7.5 4.7
	569 526.5 518.5 512	476 476 474	4 4 4 6 9 4 6 9 6 9	469 469 468.5	468 464.5 463.5	461.5 459 452 452
@@@@CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	26 28 29	310		3 3 3 3 4	39 410 41	4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

## ALIGNMENTS

Proteins controlling cell migration and cell death and their encoded DNAs, applicable in developing drugs for treating or suppressing cancer or tumor metastasis or as regulators of cell migration for L-FILIP, S-FILIP, filamin-interacting protein; cell migration; cell death; cytostatic; neuroprotective; immunosuppressive; cancer; tumour metastasis; transplantation therapy. (NISC-) JAPAN SCI & TECHNOLOGY CORP. ABP97029 standard; protein; 1212 AA. Rat L-FILIP protein SEQ ID NO:2. 29-JUL-2002; 2002WO-JP007676. 27-AUG-2001; 2001JP-00256910. (first entry) WPI; 2003-268423/26. Sato M, Nagano T; Rattus norvegicus. N-PSDB; ACC45354. WO2003018804-A1. 18-JUN-2003 06-MAR-2003. ABP97029; RESULT 1 **ABP97029** 

Claim 1; Page 54-60; 96pp; Japanese.

transplantation.

The present sequence represents rat L-FILIP which is a filamininteracting protein. L-FILIP has a function of controlling cell migration
and cell death. L-FILIP has cytostatic, neuroprotective and
immunosuppressive activities. The L-FILIP protein can be used for
controlling cell migration and cell death, which is applicable in
developing drugs for treating or suppressing cancer or tumour metastasis
or as regulators of cell migration for transplantation therapy, and also
for controlling the mobility and cell death of nerve cells, promoting
decomposition of the actin-binding protein e.g. filamin-interacting
protein in the treatment of preiventrilcular nodular heterotopia

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, nootropic, immunosuppressant, cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
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Zhao
                                                                                                                                                                                                                     1081 AAEGVSPVITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTRG
                                                                                                                                                                                              TQSVSGQDGSSQRPTPTRIPMSKGMKAGKPVVAASGAGNLTKFQPRAETQSMKIELKKSA
SQKPKSADPTLGPERAMSPVTITTISREKSPEGGRSAFADRPASPIQIMTVSTSAAPTEI
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ΑJ,
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Wehrman T, Xu C,
R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAM40016 standard; protein; 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 3161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999; 99US-00471275.
21-57M-2000; 2000US-00585217.
25-4DN-2000; 2000US-00552317.
26-4UN-2000; 2000US-0058042.
19-4UN-2000; 2000US-00620312.
03-AUG-2000; 2000US-0065450.
14-5EP-2000; 2000US-0065450.
19-CCT-2000; 2000US-0063191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Asundi V,
Wang Z, Wehrman T,
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                                                                                                                                                                                                                                                                                1201 ASSTASLGGGKG 1212
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J, Wang Z, Wehr
P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442253/47.
N-PSDB; AAI59172.
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                                                                                                                                              MRSRNQGGESSSNGHVSCPKSSIISSDGGKGPSEDAKKNKANRKEEDVMASGTIKRHLKP
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                                                                 Length 1212;
                                                               Score 6082; DB 6;
Pred. No. 1.2e-303;
Mismatches 0;
                                                               Query Match
100.0%; Sc
Best Local Similarity 100.0%; Pi
Matches 1212; Conservative 0;
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bystem, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's. Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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                                                                                                                                                                                                                                                                                    PSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEP
                                                                                                                                                                                                                                                                                                 61 TSGECERKTKKSLELSKEDLIQLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEP
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                                                                                                                                                                                                         Gaps
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                                                                                                                                                                           93.7%; Score 5696.5; DB 4;
93.5%; Pred. No. 7.1e-284;
ive 37; Mismatches 41;
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Matches 1134; Conservative
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interacting protein. L-FILIP has a function of controlling cell migration
and cell death. L-FILIP has cytostatic, neuroprotective and
immunosuppressive activities. The L-FILIP protein can be used for
controlling cell migration and cell death, which is applicable in
developing drugs for treating or suppressing cancer or tumour metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins controlling cell migration and cell death and their encoded DNAs, applicable in developing drugs for treating or suppressing cancer or tumor metastasis or as regulators of cell migration for
                                                                                                                                                                                                    1021 IAVSPESQEMPMGRTILKVTPEKQTVPTPVRKYNSNANIITTEDNKIHIHLGSQFKRSPG
                                                                                                                                                                                                                                                            GTQSVSGQDGSSQRPTPTRIPMSKGMKAGKPVVAAAPGAGNLTKFEPRAETQSMKIELKKS
                                                                            961 MPQKQKSGDTTLGPERAMSPVTITTFSREKTPESGRGAFADRPTSPIQIMTVSTSAAPAE
VGLKKPMERSSVLDRYPPAANELTMRKSW1PWMRKRENGPSTPQEKGPRPNQGAGHPGEL
                 841 VGLKKPVERSSVLDRYPPAANELTMRKSWIPWMRKRENGPSITQEKGPRTNSSPGHPGEV
                                                         VLAPKQGQPLHIRVTPDHENSTATLEITSPTSEFFSSTTVIPTLGNQKPRITIIPSPNV
                                                                                                                      MSQKPKSADPTLGPERAMSPVTITTISREKSPEGGRSAFADRPASPIQIMTVSTSAAPTE
                                                                                                                                                                                 1020 IAVSPESQEVPMGRTILKVTPEKQTVPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSPG
                                                                                                                                                                                                                                            1080 PAAEGVSPVITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTR
                                                                                                                                                                                                                                                                                                         GTQSVSGQDGSSQRPTPTRIPMSKGMKAGKPVVAASGAGNLTKFQPRAETQSMKIELKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-FILIP; S-FILIP; filamin-interacting protein; cell migration; cell death; cytostatic; neuroprotective; immunosuppressive; cancer; tumour metastasis; transplantation therapy.
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N-PSDB; ACC45356.
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961 MPQKQKSGDTTLGPERAMSPVTITTFSREKTPESGRGAFADRPTSPIQIMTVSTSAAPAE 1020
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                                                                                                 IAVSPESQEVPMGRIILKVTPEKQTVPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSPG 1079
                                                                                                                                                                                                                                                   The present sequence represents rat S-FILIP which is a filamin-interacting protein. S-FILIP has a function of controlling cell migration and cell death. S-FILIP has a function of controlling cell migration cell death, is applicable in controlling cell migration and cell death, which is applicable in cooling action and cell death, which is applicable in developing drugs for treating or suppressing cancer or tumour metastasis or as regulators of cell migration for transplantation therapy, and also for controlling the mobility and cell death of nerve cells, promoting decomposition of the actin-binding protein e.g. filamin-interacting protein in the treatment of preiventrilcular nodular heterotopia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins controlling cell migration and cell death and their encoded DNAs, applicable in developing drugs for treating or suppressing cancer or tumor metastasis or a regulators of cell migration for
                                                                                                                         IAVSPESQEMPMGRTILKVTPEKQTVPTPVRKYNSNANIITTEDNKIHIHLGSQFKRSPG
   901 VLSPKQGQPLHIRVTPDHENSTATLEITSPTSEEFFSSTTVIPTLGNQKPRITIIPSPNV
                                                                                                                                                                                                                                  GTQSVSGQDGSSQRPTPTRIPMSKGMKAGKPVVAASGAGNLTKFQPRAETQSMKIELKKS
                                                                                                                                                                   1080 PAAEGVSPVITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTITITTPVTTSSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-FILIP; S-FILIP; filamin-interacting protein; cell migration; cell death; cytostatic; neuroprotective; immunosuppressive; cancer; tumour metastasis; transplantation therapy.
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or as regulators of cell migration for transplantation therapy, and also for controlling the mobility and cell death of nerve cells, promoting decomposition of the actin-binding procein e.g. filamin-interacting protein in the treatment of prelventrilcular nodular heterocopia
                                                                                                                                                                                                         1 MRSRNQGGESSSNGHVSCPKSSIISSDGGKGPSEDA-KKNKANRKEEDVMASGTIKRHLK 59
                                                                                                                                                                                                                                                                          61 TSGECERKTKKSLELSKEDLIQLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEP
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93.7%; Score 5696.5; DB 6;
Best Local Similarity 93.5%; Pred. No. 7.1e-284;
Matches 1134; Conservative 37; Mismatches 41;
                                                                                   Sequence 1213 AA;
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                                                                                          RFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAEEELQELREKIAK
                                                                                                                                      GECGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRLEVEKL
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  Length 965;
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6.1e-240;
79.5%; Score 4838; E
100.0%; Pred. No. 6.1
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602 complementary strand of a polynucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a coligonucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in specification and/or disgnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13612 to AAH13613 represent human amino acid sequences; and AAH13612 to AAH13612 represent coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy
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T;
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Otsuki
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llarity 92.3%; Pred. No. 2e-148;
Conservative 19; Mismatches 31;
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A, Nagai K,
                                                                                                                                                    protein sequence SEQ ID NO:11924
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T, Wakamatsu
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999; 99JP-00248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-2000; 2000JP-00241899
                                   standard; protein;
                                                                                                             26-JUN-2001 (first entry)
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                                                                                                                                                                                                                              Homo sapiens
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Best Local Simi
Matches 603;
                                                                                                                                                                                                                                                                                                       07-FEB-2001
                                   AAB93085
                                                                         AAB93085;
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120 739 180 799 240 859 300 919 360 979 420

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Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                     Human protein sequence SEQ ID NO:12253
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AAB93244 standard; protein; 551
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29-JUL-1999; 99JP-00248036. 27-ANG-1999; 9JP-0030253. 11-JAN-2000; 2000JP-00118776. 02-MAX-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899.

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(HELI-) HELIX RES INST.

Yamamoto J; Isogai T, Nishikawa T, Hayashi K, Saito K, Ya Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; s,

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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the
complementary strand of a polymucleotide which comprises one of the 5602
cucleotide sequences defined in the specification, where the
nucleotide sequences defined in the specification, where the
cuplementary strand of a polymucleotide which complementary to the
complementary strand of a polymucleotide which complementary to the
complementary strand of a polymucleotide which complementary to a
polymucleotide comprises a 3'-end sequence complementary to a
polymucleotide comprises a 1'-end sequence complementary to a
polymucleotide which comprises a 1'-end sequence, where the
coligonucleotide comprises a 1'-end sequence of an endiance in the
specification. The primer sets can be used in antisense therapy and in
complementary full-length cDNAs. The primers are also useful for the
complementary full-length cDNAs. The primers are also useful for the
complementary without any specialised methods. AAH0316 to AAH03628
represent human amino acid sequences; and AAH03629 to AAH03628
represent human amino acid sequences; and AAH03629 to AAH03628
present invention
                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                              Claim 8; SEQ ID NO 12253; 2537pp + Sequence Listing; English.
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Sequence 551 AA;

1099

540

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120
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                                            248 MLVDEROMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKLLKLEVDFEHKAS 307
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                                                                                                     61 RFSQEHEEMNAKLANQESHNRQLRLKLVGLTQRIEELEETNKNLQKAEEELQELRDKIAK
                                                            1 MLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAITSKSKEDRQKLLKLEVDFEHKAS
                                                                                       308 RFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAEEELQELREKIAK
                                                                                                                                                QKRMSELEKLEEAFSRSKSECTQLHINLEKEKNLTKDLLNELEVVKSRVKELECSESRLE
                                                                                                                                                                                          368 GECGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRLEVEKL
                                                                                                                                                                                                                      KAELSLKDDLTKLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLI
                                                                                                                                                                                                                                     TEQDKANFLSQQLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEEAKSRDLQAEVQALK
                                                                                                                                                                                                                                                                                                                                                                                               548 EESKKILKIKSEMEEKEYSLTKERDELMGKIRSEEERSCELSCSVDLLKKRLDGIEEVER
                                                                                                                                                                                                                                                                                                          608 BINRGRSCKGSEFTCPEDNKIRELTLEIBRLKKRLQQLEVVEGDLMKTEDEYDQLEQKFR
                                                                                                                                                                                                                                                                                                                         ;
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  Length 551;
Query Match
42.5%; Score 2586; DB 4; Length 551
Best Local Similarity 94.7%; Pred. No. 1.2e-124;
Matches 521; Conservative 19; Mismatches 10; Indels
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989 KSPEGGRSAFADRPASPIQIMTVSTSAAPTEIAVSPESQEVPMGRTILKVTPEKQTVPAP 1048
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                                                                                                                             349 EELQDIKEKISKGEYGNAGIMAEVEELRKRVLDMEGKDEELIKMEEQCRDLNKRLERETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEAKSGHLSREVDALKEKIHEYMATEDLICHLQGDHSVLQKKLNQQENRNRDLGREIENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||| ::|::|||| |||||| || || ||||| || TKELERYRHFSKSLRPSLNGRRISDPQVFSKEVQTEAV----DNEPPDYKSLIPLERAV
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                                                                     416 HSKELRLEVEKLOKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNBLEVVKSR
                                                                                                                                                                                                                                                                                                476 VKELECSESRLEKAELSLKDDLTKLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNFKVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      823 INGOLYEESENOD-----EDPNDEGSVLSFKCSOSTPCPVN----RKLWIPWMKSK
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  SAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCH
                                                        RRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQARKEKENAKL
                                                                                                             RDELVKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKL
                                                                                                                                                                    LKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAE
                                                                                                                                                                                                                         EELQELREKIAKGECGNSSLMABVESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the protein sequence of GIP130b, a novel 130 kDa Goodpasture antigen binding protein (GPBP) interacting protein. The DOC/GIP90/130 mRNA family results from a complex diversification mechanism operating on the expression of the GIP90 gene on chromosome 3 (3q12). GIP90/130 polypeptides of the invention interact with GPBP and are capable of aggregation. They can be used to modify GPBP-GIP90/130 interactions, to modify GP90/130 aggregation, and to modulate gene expression. The invention provides GIP90/130 polypeptides, portions of them, antibodies, nucleic acid sequences, expression vectors and host chells, as well as methods for detecting GIP90/130 polypeptides and nucleic acids, and methods for treating an autoimmune disease or cancer by modifying the expression or activity of one or more GIP90/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goodpasture antigen binding protein interacting protein, GPBP, GIP130b, human; transcription factor; autoimmune disease; cancer;
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46.2%; Pred. No. 2e-117;
ive 214; Mismatches 337; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Page 78-83; 115pp; English.
                                                                                              standard; protein; 1133
                                                                                                                                                                                GPBP-interacting protein GIP130b.
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Local Similarity 46.2%; Pre
hes 542; Conservative 214;
                                                                                                                                                                                                                                       immunosuppressive; cytostatic.
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20-MAY-2002; 2002US-0382004P.
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REVERT-ROS F.
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SVNGKRMVDV
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N-PSDB; ACC83929.
SGNGRRMVDV
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1049 VRKYNSNANIITTEDNKIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTAEKEVSTGTVL 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGKVMDVTEKLIEESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLL 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  989 KSPEGGRSAFADRPASPIQIMTVSTSAAPTEIAVSPESQEVPMGRTILKVTPEKQTVPAP 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 822 FIRKSFOE-ENHIMSNLRQVGLKKPMERSSVL----DRYPPAANELTMRKSWIPWMRKR 875
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                                                                                                                                                                                                               RRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQARKEKENAKRLNKL
                                                                                       236 RDELVKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKL
                                                                                                                        296 LKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAE
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polypeptides, useful for diagnosing and/or treating disorders associated
with the GIP90/130 polypeptide, such as autoimmune disorders and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of GIP130c, a novel 130 kDa Goodpasture antigen binding protein (GBPB) interacting protein. The DOC/GIP90/130 mRNA family results from a complex diversification mechanism operating on the expression of the GIP90 gene on chromosome 3 dre capable of 1909 gene on chromosome 3 are capable of aggregation. They can be used to modify GBP-GIP90/130 polyapetides of the invention interact with GBPs and interactions, to modify GBP0/130 aggregation, and to modify GBP0/130 polyapetides, portions of them, antibodies, nucleic acid sequences, expression vectors and host oncells, as well as methods for detecting GIP90/130 polyapetides and host nucleic acids for detecting GIP90/130 polyapetides and host nucleic acids methods for treating an autoimmune disease or cancer polyapetides
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                                                                                                                                                                                                                                     Goodpasture antigen binding protein interacting protein; GPBP, GIP130c, human; transcription factor; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 1133;
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40.2%; Score 2444.5; DB 6.
Best Local Similarity 46.1%; Pred. No. 5.2e-117;
Matches 541; Conservative 214; Mismatches 338;
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                                                                                                                                                                                            GPBP-interacting protein GIP130c.
                                                      ABR62253 standard; protein; 1133
                                                                                                                                                                                                                                                                 human; transcription factor; au
immunosuppressive; cytostatic.
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(REVE/) REVERT-ROS F.
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N-PSDB; ACC83930.
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          RESULT B
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                                                                         289 TRLEKELQTQTTKFHQDQDTIMAKLTNEDSQNRQLQQKLAALSRQIDELEETNRSLRKAE
                                                                                                                                                                                                                  | || :| :| :| :| :| || || KNRLQSLEAIEKDFLKUKLKLKLKDRKAIEDD
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                                                                                                                                             416 HSKELRLEVEKLOKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSR
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                                                     LKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAE
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protein; 893
 Human CGDD-51 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or
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                                                                                                       GPBP; GIP130a;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1135;
                                                                                                   Goodpasture antigen binding protein interacting protein, human; transcription factor; autoimmune disease; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 68-72; 115pp; English
                                                                  GPBP-interacting protein GIP130a.
                                                                                                                                        immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001US-0338287P.
20-MAY-2002; 2002US-0382004P.
                                                                                                                                                                                                                                                                                05-DEC-2002; 2002WO-EP013802
                                                                                                                                                                                                                                                                                                                                                                                                                           Saus J, Revert-Ros F;
                                                                                                                                                                                                                                                                                                                                                                                        REVERT-ROS F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-505281/47.
N-PSDB; ACC83928.
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Best Local Similarity
Matches 541; Conserv
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                                                                                                                                                                                                            WO2003048193-A2
                                                                                                                                                                                                                                                                                                                                                                     (SAUS/) SAUS
(REVE/) REVER
                                                                                                                                                                           Homo sapiens.
                                 22-SEP-2003
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ABR62251;
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The invention relates to an isolated polypeptide associated with cell growth, differentiation and death (GGDD). Also disclosed are the growth, differentiation and death (GGDD). Also disclosed are the polymelectides encoding the polypeptides. The polypeptides and conditions associated with the decreased expression or over expression of CGDD. Such diseases include cell proliferative (e.g. expression or over cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and reproductive disorders, or disorders of the placenta. They are also reful in assessing the effects of exogenous compounds on the expression of muclaic acid and amino acid sequences of GGDD. The CGDD or its confined acid and amino acid sequences of GGDD. The CGDD or its agonist or antagonist of the polypeptides, or in altering the expression of the target polymulectide and compounds that specifically bind to or of the target polypeptide and compounds that specifically bind to or of meaning the expression of procein-protein interactions, drug-target in monitoring or measuring procein-protein interactions, drug-target in monitoring or measuring corporates in profiles. Sequences given in records AAR69667 expression profiles. Sequences given in records AAR69667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human proteins associated with cell growth, differentiation, and death (CGDD), useful for diagnosing, treating and preventing diseases conditions associated with the aberrant CGDD expression e.g. cancer, AIDS, or epilepsy.
         Human, cytostatic, antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective; anti-HTV; antiallergic, antinflammatory, synaecological, cancer; atherosclerosis, epilepsy, Huntington's disease, erroke, AIDS, allergy; placenta, reproductive, CGDD, cell growth, cell differentiation; cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Chawla NK; Elliott VS, Emerling BM, Gandhi AR, Gietzen KJ, Gorvad AE; Griffin JA, Hafalia AJA, Ison CH, Kable AE, Kalafus DP; Lebr-Mason PM, Marquis JP, Nguyen DB, Ramkumar J; Richardson TW, Sapperstein SK, Swarnakar A, Tang YT, Tran UK; Warren BA, Xu Y, Yao MG, Yue H, Yue H;
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05-0CT-2001, 20010S-032180P.
26-0CT-2001, 20010S-0348186P.
26-0CT-2001, 20010S-0348165P.
02-NOV-2001, 20010S-0348186P.
09-NOV-2001, 20010S-034818P.
09-NOV-2001, 20010S-034518P.
09-NOV-2001, 20010S-034518P.
09-NOV-2001, 20010S-034518P.
07-DEC-2001, 20010S-0337375P.
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Best Local Similarity 46.03
Matches 424; Conservative
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N-PSDB; ACC90628.
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                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                              784 ALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP-----AVFIRKSFQE-ENH 832
                                                                                                                                                                                                                                                                                                                                      SLRPSLNGRRISDPQVFSKEVQTEAV----DNEPPDYKSLIPLERAVINGQLYEESENQ
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                                                                                                                                                                                                                                                                                              RRYANERDKAQFLSKELEHVKMELAKYKLAEKTE-TSHEQWLFKRLQEEEAKSGHLSREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                              884 EKGPRPNQGACHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTS--EFFSSTTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEDNKIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 MLVDEROMHIEQLGLQSQKVQDLTQKLREBEBKLKAVTYKSKEDRQKLLKLEVDFEHKAS
           RFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAEEELQELREKIAK
                                                                                        OKRMSELEKLEEAFSRSKSECTOLHLNLEKEKNLTKDLLNELEVVKSRVKELECSESRLE
                                                                                                                                 EESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKRLDGIEEVER
                                                                              GECGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRLEVEKL
                                                                                                                                                            KAELSLKDDLTKLKSFTVMLVDERKONMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLI
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31.7%; Score 1926; DB 6; Length 893; 46.0%; Pred. No. 1.6e-90; ive 168; Mismatches 266; Indels 6

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New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or
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                     229 KEELTKLKSFALMVVDEQQRLTAQLTLQRQKIQELTTNAKETHTKLALAEARVQEEEQKA
                                                                                 409 QSKDFKLEVEKLSKRIMALEKLEDAFNKSKQECYSLKCNLEKERMTTKQLSQELESLKVR
                                                                                                                                                                                                                                                                           ONKVITVIEKLIEETKRALKSKIDVEEKMYSVIKERDDLKONKLKAEEEKGNDLLSRVNML
                                                                                                                                                                                                                                                                                                                                                                                                         296 LKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAE
                                                                                                                                EELQELREKIAKGECGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEH
                                                                                                                                                                                                                                                        476 VKELECSESRLEKAELSLKDDLTKLKSFTVMLVDERKNMMEKIKQBERKVDGLNKNPRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      652 LMKTEDEYDQLEQKFRTEQDKANFLSQQLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRL
   236 RDELVKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKL
                                                                                                                                                                                            416 HSKELRLEVEKLOKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSR
                                                                                                                                                                                                                                                                                                                         QGKVMDVTEKLIESSKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLL
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20-MAY-2002; 2002US-0382004P.
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REVERT-ROS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGESEK----KTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYG 115
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                                                                                                                                                                                                                                                                                                                                                                                                   New Goodpasture antigen binding protein-interacting 90 and 130 kDa
polypeptides, useful for diagnosing and/or treating disorders associated
with the GIP90/130 polypeptide, such as autoimmune disorders and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRSRNQGGESSSNGHVSCPKSSIISSDGGKGPSEDAKKNKANRKEE-DVMASGTIKRHLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodpasture antigen binding protein interacting protein; GPBP; GIP90; human; transcription factor; autoimmune disease; cancer;
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30.1%; Score 1828; DB 6; Length 764;
Best Local Similarity 50.7%; Pred. No. 1.4e-85;
Matches 386; Conservative 144; Mismatches 210; Indels 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 59-62; 115pp; English.
 GPBP-interacting protein GIP90
                                                             immunosuppressive; cytostatic.
                                                                                                                                                                                         05-DEC-2002; 2002WO-EP013802
                                                                                                                                                                                                                       07-DEC-2001; 2001US-0338287P.
20-MAY-2002; 2002US-0382004P.
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                                                                                                                                                                                                                                                                      (SAUS/) SAUS J.
(REVE/) REVERT-ROS F.
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                                                                                                                           WO2003048193-A2.
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                                                                                             Homo sapiens
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Sequence 752 AA;
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                                          The present sequence is that of a 785-amino acid polypeptide that is present in the novel Goodpasture antigen binding protein (GPBP) interacting protein GIPP130 (Gee ABRE2251). The polypeptide lacks critical regions of GIPP9(130 polypeptides) implicated in GPBP interaction and induction of gene expression, but contains sequences that downergulate interaction with GPBP. The polypeptide, or antibodies to it, can be used to modify GPBP-GIP90/130 polypeptide interactions or to modify GIP90/130 polypeptides aggregation. The invention provides GIP90/130 polypeptides, portions of them, antibodies, nucleic acid sequences, expression vectors and host cells, as well as methods for detecting GIP90/130 polypeptides and nucleic acids, and methods for treating an autoimmune disease or cancer by modifying the expression or activity of one or more GIP90/130 polypeptides
                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                        358 LQELREKIAKGECGNSSLMAEVESLRKRVLEMEGKDEFITKTEAQCRELKKKLQEEEHHS 417
                                                                                                                                                                                                                                                                                                                                                      653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 RLQSLEAIEKDFLKNKLNQDSGKSTTALHQENNKIKELSQEVERLKLKLKDMKAIEDDLM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKSGHLSREVDALKEKIHEYMATEDLICHLQGDHSVLQKKLNQQENRNRDLGREIENLTK 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         932
                                                                                                                                                                                                                                                                                                                                     KELRLEVEKLOKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSRVK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                  KUMDVTEKLIEESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKK 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTEDEYDQLEQKFRTEQDKANFLSQQLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEE 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTK 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| : :|::||| ||||| | | | | | ||||| || ELERYRHFSKSLRPSLNGRRISDPQVFSKEVQTEAV----DNEPPDYKSLIPLERAVIN 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EFFSSTTVIPTLGNOKPRITIIPSPNVMSQKPK-SADPTLGPERAMSPVTITTISREKS 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP-----AVFI 823
                                                                                                                                                                                                                                                                                                      ELECSESRLEKAELSLKDDLTKLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNFKVEQG
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                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                        Query Match 27.5%; Score 1675; DB 6; Length 785; Beet Local Similarity 45.9%; Pred. No. 1e-7; Indels 4; Matches 373; Conservative 143; Mismatches 232; Indels 64;
                       Claim 34; Page 102-106; 115pp; English.
                                                                                                                                                                                                                  Sequence 785 AA;
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The present invention relates to a method for diagnosing breast cancer in a subject suspected of having endometrial cancer. The method comprises determining the expression of a set of human genes or expression products in an endometrial sample suspected of being cancerous. The human genes of the invention are differentially expressed in breast tumours characterised as high or low MAI (mitotic activity index). These sets of genes can be used to discrimiate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analyzing the expression of the human genes and their protein products. The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimes, and identification of compounds useful for the treatment of endometrial cancer. ANU84361 represent the human proteins of the invention that are differentially expressed in breast cancer tissue
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697 SNSNSSSVITTEDNKIHIHLGSPYMQA---VASPVRPASPSAPLQDNRTQGLINGALNKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein DOC1 differentially expressed in breast cancer tissue.
                                                                                                                 PRNHLSSRPGASKVTSTITITPVTTSSTRGTQ 1142
                                                                                                                                                                      Claim 37; Page 141-143; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
(BAAK/) BAAK J.
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                -----EELIKMEEQCRDLNKRLERETLOSKDFKLEVEKL
                                            DALKEKIHEYMATEDLICHLOGDHSVCKKKLNQOENRNRDLGREIENLTKELERYRHFSK
                                                                                                                                                                                                                             SLRPSLNGRRISDPQVFSKEVQTEAV.---DNEPPDYKSLIPLERAVINGQLYEESENQ
                                                                                                                                                                                                                                                            D-----BDPNDEGSVLSFKCSQSTPCPVN----RKLMIPWMKSKEGHLQNG-----
                                                                                                                                                                                                                                                                                                                    GECGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRLEVEKL
                                   QKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSRVKELECSESRLE
                                                                 KAELSLKDDLTKLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLI
                                                                                               EESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKRLDGIEEVER
                                                                                                                          EINRGR----SCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDLMKTEDEYDQLE
                                                                                                                                    QKFRTEQDKANFLSQQLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEEAKSRDLQAEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer cell marker protein SEQ ID NO:48
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2001US-0298159P.
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                     GEYGNAGIMAEV
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13-JUN-2001;
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ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
given in ABR92047 to ABR92164. A higher level of expression of (I) than
normal indicates the presence of cervical cancer. Also described: (I) a
vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
assessing (MI) whether a patient is afflicted with cervical cancer,
comprising comparing the level of expression of a marker in a patient's
ample, and the normal level of expression of the marker in a control non
cervical cancer sample, where a significant increase in the level of
expression of the marker in the patient's sample relative to that in the
cervical cancer. (I) has cytostatic activity, and can be used in gene
therapy and in vaccines. (I) is useful in detecting, characterising,
creventing and treating human cervical cancers. (I) may also be used in
various prognostic assays, pharmacogenomics and in
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                                                                                                                                                                                                                                                                                   New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKLLKLEVDFEHKAS
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Pred. No. 3.2e-76;
0; Mismatches 216; Indels
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                                                                                                                 Kamatkar
                                                                                                              Monahan JE,
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                                                                                                              Schlegel R, Chen Y, Zhao X, Monahi
Gannavarapu M, Glatt K, Hoersch S;
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Matches 363; Conservative 140;
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14-NOV-2001; 2001US-0335936P.
                                                     MILLENNIUM PHARM INC
                                                                                                                                                                                                  WPI; 2003-156967/15.
N-PSDB; ACF12851.
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Page 14

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942 PTLGNOKPRITIIPSPNVMSQKPK-SADPTLGPERAMSPVTITTISREKSPEGGRSAFAD 1000
784 ALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP-----AVFIRKSFQE-ENH 832
                           SLRPSLNGRRISDPQVFSKEVQTEAV----DNEPPDYKSLIPLERAVINGQLYEESENO 580
                                                       833 IMSNLRQVGLKKPMERSSVL----DRYPPAANELIMRKSWIPWMRKRE----NGPSTPQ 883
                                                                                   581 D-----EDPNDEGSVLSFKCSQSTPCPVN----RKLWIPWMKSKEGHLQNG----- 622
                                                                                                               884 EKGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTSE--EFFSSTTVI 941
                                                                                                                                  623 KWQTKPNANFVQPGDLVLSHTPGQPLHIKVTFDHVQNTATLEITSPTTESPHSYTSTAVI 682
                                                                                                                                                                                          683 PNCGTPKQRITILQNASITPVKSKTSTEDLANLEQGASPITMATFARAQTPESCGSLTPE 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang D;
, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, nootropic; immunosuppressant; cytostatic; gene therapy; cancer; geripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemocactic; chemockinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren F, Wa
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Asundi V, Chen R, Ma Y, Qian XB, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                               AAM41802 standard; protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Human polypeptide SEQ ID NO 6733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999; 99US-00471275.
21-JAR-2000; 2000US-00488725.
25-ARR-2000; 2000US-0552317.
20-UIN-2000; 2000US-0658042.
19-UIL-2000; 2000US-06620312.
03-AUG-2000; 2000US-0663450.
14-SEP-2000; 2000US-0663191.
19-CCT-2000; 2000US-0663191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US034263.
                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia.
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Zhou P,
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

Example 2; SEQ ID NO 6733; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,

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ί,
immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, cancer disgnosis and therapy, drug screening, and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TSGECERKTKKSLELSKEDLIQLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEP 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRSRNQGGESSSNGHVSCPKSSIISSDGGKGPSEDA-KKNKANRKEEDVMASGTIKRHLK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 MRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAKKKKKSNRKEDDVMASGTVKRHLK 67
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es 206; Conservative
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Search completed: September 7, 2004, 13:13:17 Job time : 158 secs

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September 7, 2004, 13:10:44 ; Search time 35 Seconds (without alignments) 1787.734 Million cell updates/sec
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6082
1 MRSRNQGGESSSNGHVSCPK......KIELKKSAASSTASLGGGKG 1212
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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6: /cgn2\_6/ptodata/2/iaa/pCTUS\_COMB.pep:\*

Issued\_Patents\_AA:\*

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Sequence 148, App Sequence 148, App	Sequence 15754, A Sequence 2, Appli Sequence 3, Appli	Sequence 296, App Sequence 4, Appli Sequence 1, Appli	Sequence 24, Appl Sequence 4, Appli	726	Sequence o, Appli Sequence 6, Appli Sequence 1, Appli	736 18, 32,
US-08-592-126-148 US-09-168-595-148	US-09-866-108A-15754 US-08-685-871-2 US-09-866-108A-3	US-09-976-594-296 US-08-685-576-4 US-08-685-576-1	US-09-392-714-24 US-08-533-306A-4	US-08-742-923A-4 US-09-976-594-726	US-08-533-306A-6 US-08-742-923A-6 PCT-US93-03077-1	US-09-976-594-736 US-09-010-147B-18 US-08-714-741-32
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28	3310	3 3 3 5 4 5 5 5	36 37	8 6 6	4 4 4 1 2	4 4 4 6 4 4 0

## ALIGNMENTS

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APPLICANT: Hasegawa, Kazuhide
APPLICANT: Hasegawa, Kazuhide
APPLICANT: Hasegawa, Kazuhide
APPLICANT: Arakawa, Emi
APPLICANT: Oda, Shoji
APPLICANT: Oda, Shoji
APPLICANT: Matsuda, Yuzuru
APPLICANT: Takahashi, Kacuhito
APPLICANT: Sugahara, Matchihiro
APPLICANT: Sugahara, Matchihiro
APPLICANT: Sugahara, Harva
APPLICANT: Sugahara, Harva
APPLICANT: Sugahara, Harva
APPLICANT: Sugahara, Harva
APPLICANT: Sugahara, Harva
APPLICANT: RECOMBINANT DNA COMPRISING THE RECOMBINANT DNA
TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING
TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
FILLE REPERENCE: 07898-013001
CURRENT FILLING DATE: 1997-07-25
FRIOR PLICATION NUMBER: PCT/JP96/00134
FRIOR FILLNG DATE: 1996-01-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
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Local Similarity 23.5%; Pred. No. 2.1e-17;
Les 203; Conservative 167; Mismatches 292; Indels 202; Gaps
                                                                       ; Sequence 3, Application US/08875435B ; Patent No. 6593304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TKKSVELSKEDLIQ-----
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                                                                                                                                                         GENERAL INFORMATION:
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275 REEEEKLKAVTYKSKEDR---QKLLKLEVD----FEHKASRFSQEHEEMNAKLANQESH 326
                                                                                                                                                              327 NRQLRLKLVGL-SQRIEELEETNKSLQKAEEELQ----ELREKIAKGECGNSSLMAEVES 381
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1483 TKALSLARALEEALEAKEELERTNKMLKAEMEDLVSSKDDVGKKVHELEKSKRALETQME 1542
                                                                                        1129 SERAARNKAEKQKRDĽGEELEALKTELEDTLDTTATQQELRAKREQEVTVLKKALDEËTR 1188
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                                                     SQ----KVQDLTQKLREEEEKLKA-----VTYKSKEDRQK-----LLKLEVDFE--
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; Patent No. 5710022
; GENERAL INFORMATION:
APPLICANT: Zhu, Xueliang
APPLICANT: Lee, Wen-Hwa
; TILE OF INVENTION:
NUMBER OF SEQUENCES: 8
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                                                                                                                            -HKA--SRFSQEHEEMNAKLANQ-
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APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
APPLICANT: Ishiyama, Haruo
TITLE OF INVENTION: ROOMBINANT DNA COMPRISING DNA CODING
TITLE OF INVENTION: VECTOR DNA, MICROORGANSIM CARRYING THE RECOMBINANT DNA, AN
TITLE OF INVENTION: VECTOR DNA, MICROORGANSIM CARRYING THE RECOMBINANT DNA, ANI
TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: POSPB-013001
CURRENT APPLICATION NUMBER: US/08/875,435B
PRIOR APPLICATION NUMBER: PCT/JP96/00134
PRIOR FILING DATE: 1996-01-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FABLSEQ for Windows Version 4.0
                                                                                                                          1471
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846 QVTRQEEEMQAKEDELQKIKERQQKAESELQELQCKHTQLSEEKNLLQEQLQAETELYAE 905
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                                                                                                             DGIEEVEREINRGRSCKGSEF
                                                                                        -----RELTLEIERLKKRLQQLEVVEGDL-MKTEDEY
                                                                                                                                                             DQLEQKFRTEQDKANFLSQQLE---EIKHQMAKHKAIEKGE---AVSQEAELRHRFRLEE
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7.3%; Score 445; DB 4; Length 1972;
Best Local Similarity 21.5%; Pred. No. 3.5e-17;
Matches 248; Conservative 164; Mismatches 333; Indels 406;
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                 DELMGKLRSEERSCELSCSVDLLKKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08875435B Patent No. 6593304 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T: Oda, Shoji
T: Matsuda, Yuzuru
T: Takahashi, Katsuhito
T: Sugahara, Michihiro
T: Ishiyama, Haruo
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                                                                                      TCPED-----NKI----
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LEAENSKGEVETLKAKIEGMTQSLRGLEDVVTIRSEKENLTNELQKEQERISELEIINS 1784
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                                                   ---SLKDDLTKLKSFTVMLVDERKNMMEKIKQEERKVDGL---NK
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: YEN, TIMOTHY J.
APPLICANT: YEN, TIMOTHY J.
TITLE OF INVENTION: TRANSIBINILY-EXPRESSED KINETOCHORE PROTEIN, TITLE OF INVENTION: TRANSIBINILY-EXPRESSED KINETOCHORE PROTEIN, TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE DANN, DORFWAN, HERRELL AND SKILLMAN
STREET: 1601 MARKET STREET, SUITE 720
CITY: PHILADELPHIA
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1205 KENSDLSEKLEYFSCDHQELLQRVETSEGLNSDLEMHADKSSREDIGDNVAKVNDSWKER 1264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 I-----GE-DVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTVYELENEKH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------LKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 LEETINKSLQKAEEELQELREKIAKGECGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQC 403
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                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC Compatible
COMPUTER: TBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/1239
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: US 08/141,239
FILING DATE: 22-OCT-1993
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-CJ 1191
TELECOMMUNICATION INFORMATION:
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                                                                            Suite 700
                                  ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive,
CITY: San Diego
STATE: California
                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-328-254-6
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Best Local S:
Matches 275
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2664 KIQVLQSKNASLQDTLEVLQSSYKNLENELELTKMDKMSFVEKVNKMTAKETELQREMHE 2723
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2453 LEAENSKGEVETLKAKIEGMTQSLRGLELDVVTIRSEKENLTNELQKEQERISELEIINS 2512
                                                                                                                                                                                                                                                                     -----OKLEKKDEEISRLKNQIQDQEQLVSKLSQVEGEHOLWKEQNLELRNLTVELEQ 2663
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                                                                                                                                                                                                                                                                                                                       665 KFRTEQDKANFLSQQLEEIKH------QMAKHKAIEK-GEAVSQEAELRHRFRL 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTMRKSWIPWMRKRENGPSTPQEKGPRPNQGAGHPGELVLAPKQGQPLHIRV---TPDHE 918
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                                                                                                                                                                                                                                                                                                                                                                                                             712 EEAKSRDLQAEVQALKEK-----IHELMNKEDQLSQLQVDYSVLQQRF----MEEET 759
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GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid Encoding a Transiently
TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                     -- REINRGRSCKGS
                                                                                                                                                                                2557 QÉ-ACKAKEQNÍSSQVECÍELEKAQLÍQGLDEAKNNYIVLQSSVKGLIQEVEDĞK----
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1601 Market Street Suite 720
                                             NFKVEQGKVMDVTEKLIEESKKLLKLKSEMEEKEYSLT
                                                                                                                                     EERSCE----LSCSVDLLK----KRLDGIEEVE---
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ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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|KENSDLSEKLEYFSCDHQELLQRVETSEGLNSDLEMHADKSSREDIGDNVAKVNDSWKER 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 KHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQA----RKEKEN-AKRLNKLRDELVK- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.1%; Score 433; DB 1; Length 3248; Best Local Similarity 20.1%; Pred. No. 3.1e-16; Matches 270; Conservative 228; Mismatches 454; Indels 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 KKSVELSK------EDLIQLLSIMEG------ELQAREDV-
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                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,700
FILING DATE: 09-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, JANET E.
REGISTRATION NUMBER: 36,252
                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bingle
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TOPOLOGY: lin
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2557 QE-ACKAKEQNLSSQVECLELEKAQLLQGLDEAKNNYIVLQSSVKGLIQEVEDGK---- 2610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2784 KBGKVREBIAEYQLRLHEAEKKHQALLLDTNKQYEVEIQTYREKLTSKEECLSSQKLE-- 2841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2513 SF-----ENILQE----KEQEKVQMKEKSSTAMEMLQTQLKELNERVAALHND 2556
                                                                                                                                                                                                                                                                                                                                                                                                                   2724 MAQKTAELQEELSGEKORLAGELQLLLEEIKSSKÖÖLKEĽTLENŠEĽKKSLDCMHKDQVE 2783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2941 ELKETLEEKTKEADEYLDKYCSLLISHEKLEKAKEMLETQVAHLCSQQ------ 2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                961 SQKPKSADPTLGPERAMSPVTITTISREKSPEGGRSAFADR-------PASPI 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1007 QIMTVSTSAAPTEIAVSPESQ-------EVPMGRT----ILKVTPEKQT 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3048 SFSKKSKKAVMSGIHPAEDTEGTEFEPEGLPEVVKKGFADIPTGKTSPYILRRTTMATRT 3107
                                                          582 EERSCE----LSCSVDLLK----KRLDGIEEVE-------REINRGRSCKGS 618
                                                                                                                                                              619 EFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDLMKTEDEYD-------QLEQ 664
                                                                                                                                                                                                                                                                 665 KFRTEQDKANFLSQQLEEIKH------QMAKHKAIEK-GEAVSQEAELRHRFRL 711
                                                                                                                                                                                                                                                                                                                                                                     712 EEAKSRDLQAEVQALKEK-----IHELMNKEDQLSQLQVDYSVLQQRF----MEEET 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        760 KNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1045 VPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTAEKEVST 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3108 SPRLAAQKLALSPLSLGKEN-----LAESSKPTAGGSRS----QKVKVAQRSPVDS 3154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            820 AVFIRKSFQEE--NHI------MSNLRQVG-LKKPMERS-SVLDRYPPAANE 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 LIMRKSWIPWMRKRENGPSTPQEKGPRPNQGAGHPGELVLAPKQGQPLHIRV---TPDHE 918
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Patent No. 5616500
GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Lee, Seung-Chul
APPLICANT: Chung, Soo-11
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF SEQUENCES: 117
COMPRESPONDENCES: 117
COMPRESPONDENCES: 117
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!: 620 Newport Center Drive, Sixteenth Floor
Newport Beach
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1993 FLDVENELSRIRSEKASIEHEALYLEADLEVVQTEKL--CLEKDNENKQKVIVCLEEELS 2050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2453 LEAENSKGEVETLKAKIEGMTQSLRGLELDVVTIRSEKENLTNELQKEQERISELEIINS 2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IHMLRTEKTKPE-----VLEAHYGSAEPEKVLRVLHRD------AILAQEKS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 I-----GE-DVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTVYELENEKH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 KHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQA----RKEKEN-AKRLNKLRDELVK- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 -------LKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 VIYKSKEDROKLLKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 LEETNKSLOKAEEELQELREKIAKGECGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQC 403
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----
                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Jamet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4010
TELEFAX: (215) 563-401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS: not relevant
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HYPOTHETICAL: N
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1112 REEPEKRRR------QERERQCREEELQQEEQQLREERRKRRQELERQYREEEE 1162
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                                                                       993 EEPEKRR-QEREKKYREEEELQQEEEQLLREEREKRRQEWERQYRKKDELQQEEEQLL 1051
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                                                                                                                                                                                                786 RPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETPAVFIRKSFQEENHIMSNLRQVGLKKP
                                -KIHELMNKEDOLS
                                                                                                                742 QLQVDYSVLQQR---FMEEE----TKNKNMGRE------VLNLTKELELSKRYSRAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and TITLE OF INVENTION: Mehods of Using Same NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.1%; Score 429; DB 2; Length 1898;
llarity 23.2%; Pred. No. 2.7e-16;
Conservative 168; Mismatches 376; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                         1163 LOROKRKORYRDEDORSDLKWOWEP---EKEN 1191
                                                                                                                                                                                                                                                                                  846 MERSSVLDRYPPAANELTMRKSWIPWMRKREN 877
                                  QEAELRHRFRLEEAKSRD----LQAEVQALKE-
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REGISTATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424

NPDITE: 14-FEB-1997

CLASSIFICATION: 424

NPDITE: 14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/056,200
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 94, Application US/08800644; Patent No. 5988752; GENERAL INFORMATION: APPLICANT: Lee, Seung-Chul; APPLICANT: Kim, In-Gyul; APPLICANT: Chung, Soo-Il; APPLICANT: Park, Sang-Chul; APPLICANT: Park, Sang-Chul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (714) 760-0404
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APPLICATION NUMBER: US/
FILING DATE: 14-FEB-199
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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nes 216; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 KKLLEQEKAYQARKEKENAKRINKLRDELVKLKSFALMLVDERQMHIEQLGLQSQKVQDL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 LKLEEEERREQQERREQQLRREQEERRE-QRLK------RQEBEERL---QQRLRSE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 TQKLREEEEKLKAVTYKSKEDRQKLLKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 QQLRREQEERLEQLLKREEEKR------LEQERREQRLKREQEERRDQLLKREEERRQQ 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 RLKL---VGLSORIE------ELEETNKSLOKAEEELOELREKIAKGECGNSSLMAEVE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 SLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRL----EVEKLQKRMSELEK 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495 DOLTKLKSFTVMLVDERKONMMEKIKQEBRKVD---GLNKNFKVEQGKV-MDVTEKLIEES 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933 EEREKRRRQEQERQYREEEQLLQEEEQLLREEREKRRRQERERQYRKDKKLQQKEEQLLG 992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 EDAKKNKANRKEEDVMASGTIKRHLKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.2%; Pred. No. 2.7e-16;
Matches 216; Conservative 168; Mismatches 376; Indels 172;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
FILING DATE: 30-APR.1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELEPHONE: (714) 760-0404
TELEPHONE: (714) 760-9404
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        1898 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   / MOLECULE TYPE: protein US-08-056-200-94
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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; NUMBER OF SEQ ID NOS: 180 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 11 ; LENGTH: 3878 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-914-259-11	Query Match 6.9%; Score 420; DB 4; Length 3878; Best Local Similarity 20.8%; Pred. No. 2.1e-15; Matches 238; Conservative 185; Mismatches 327; Indels 394; Gaps 47;	Qy 29 GKGPSEDAKKNRANRKEEDUWASGTIKRHLK 59	QY 60 PSGESEKKTKKSVELSKE77 : :        Db 101 SGEITSHEQGFSVELESEISTTADDCSSEVNGCSFVMRTGKPTNLLREEEFGVDDSYSEQ 160	OY 78DLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVLHRDA 130  DD 161 GAQDSPTHLEWMESELAGKQHEIEELNRELEEMRVTYGTEGLQQLQEFEAAIKQRDG 217	Qy 131 ILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRT 178	QY 179 VY211  DD 267 THSSTAADLLQAKQQIL/THQQQLEEQDHLLEDYQKKKEDFTWQISFLQEKIKVYEMEQDK 326	Qy 212KLLEQEKAYQARKEKENAKRLNKLRDELVKLK 243  Db 327 KVENSNKEEIQEKETIIEELNTKIIEEEKKTLELKDKLTTADKLLGELGEQIVQKNQEIK 386	QY 244 SFALMLVDERQMHIEQLGLGSQKVQDLTQKLREEEEKLK 282 :     :	QY 283 AVTYKSKEDRQKLLKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRL 332	QY 333 KLVGLSQRIEBLEBTNKSLQKABEBLQBLREKIAKGBCGNSSLMAEVESLRKRVLEMEGK 392    ::    :    :    :	QY 393 DEBITKTEAQCRELKKKLQEBEHHSKELRLEVEKLQKRMSELEKLBEAFSRSKSEC 448	Qy 449 TQLHLMLEKEKNLTKDLLNELEVVKSRVKELECSESRLEKABLSLKDDLTKLKS 502	QY 503 FTVMLVDERKUMMEKIKQEERKVDGLNKNFKVEGGKVMDVTEKLIEESKKLLKLK 557	Oy   558   SEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKKLDGIEEVEREINRGRSCKG   617	Oy   668TEQDKANTLS	יייי בייייי ביייייי ביייייי ביייייייייי
OY 94 EDVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAOEKSIGEDVYEKPISEL 150  1	OY 211 KKLLEQEKAYQARKEKENAKRLANKLRDELVKLKSFALMLVDERQMHIEQLGLQSQKVQDL 270	QY 271 TQKLREBEEKLKAVTYKSKEDRQKLLKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQL 330	QY 331 RLKLVGLSQRIEELEETNKSLQKABEELQELREKIAKGECGNSSLMAEVE 380 	OY 381 SLRKRVLEMEGKDEBITKTEAQCRELKKKLQEEEHHSKELRLEVEKLQKRMSELEK 436  DD 657EQEERRHEQLRREQDERREGRLKREEEEERLEGRLKREHEEERREGELAE-EE 708	OY 437 LEBAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVYKSRVKELECSESRLEKAELSLK 494	QY 495 DDLTKLKSFTVMLVDERKNPMEKIKQEERKVDGLNKNFKVEQGKV-MDVTEKLIEES 550 : :     : : :     : :     :     :	OY 551 KKLIKLKSEMEEKEYSLTKERD-ELMGKLRSEBERSCELSCSVDLIKKRLD 600 ::  :  : : :	OY 601 GI-EEVEREINRGRSCKGSBFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDLMK 654	QY 655 TEDEYDQLEQKFRTEQDKANFLSQQLEEIKHQMAKHKAIEKGEAVS 700	OY 701 QEAELRHRFRLEEAKSRDLQAEVQALKEKIHELMNKEDQLS 741	QY 742 QLQVDYSVLQQRFMEEETKNKNMGREVLANLTKELELSKRYSRAL 785 : : :           :         : :	QY 786 RPSGNGRRMVDVPVASTGVQTEAVCGDAABEETPAVFIRKSFQEENHIMSNLRQVGLKKP 845	Qy 846 MERSSVLDRYPPAANELTWRKSWIPWMRKREN 877	8 6 6 6	) APPLICANT: WILLIAEMS, MARK ) TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES ) FILE REFERENCE: 8471-010-999 ; CURRENT APPLICATION NUMBER: US/509/914,259 ; CURRENT FILING DATE: 2000-11-21	

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Qy         135 EKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLILAEKCHRRTVYELENEKHKHTD 191           Db         2 DSSVGEETLPSPSLNWANESQTE-HRKDVDEXI	QY   420   RILEYEKLOKRMSELEKLEEAFSRSSECTOLHIANEEKEKNIJTKDLIABLEBVYKSRYKEE	RESULT 11 US-09-310-187A-1 ; Sequence 1, Application US/09310187A ; Patent No. 6358751
	BESUNT 10  BESUNT 10	Query Match 6.8%; Score 413.5; DB 4; Length 1231; Best Local Similarity 21.1%; Pred. No. 1.2e-15; Matches 215; Conservative 185; Mismatches 359; Indels 261; Gaps 42;

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1697 TERSRKLABQELIETSERVQLLHSQNTSLINQKKKMESDLTQLQSEVE---BAVQECRNA 1753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 RDELVKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKA----VT----- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        919 ATENKVKNLTEEMAGLDEIIAKL-----TKEKKALQEAHQQALD------DLQAEED 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AKKNKANRKEEDVMASGTIKRHLKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQARED 95
                                                          ----HQMAKHKAIEKGEAV----SQEAELRHRFRLEBAKSRDLQAEVQALKEKIHELMNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 216; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1886;
                                                                                                                                                 EDQLSQLQVDYSVLQQRFMEE-----ETKNKNMGREVLNLTKELE 776
                                                                                                                                                                                                                                                                                          APPLICANT: Leinward, Leslie A.
APPLICANT: Visterrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: Sheridan Ross P.C.
STEEFT: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.7%; Score 407.5; DB 4; Best Local Similarity 22.7%; Pred. No. 4.6e-15; Matches 219; Conservative 171; Mismatches 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/938,105 FILING DATE:
                                                                                                                                                                                                                                             Sequence 3, Application US/08938105
Patent No. 6353151
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: CTCOK, WAINELL M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3595-
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
INFORMATION FOR SEQ ID NO: 35.
SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1700
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CO
COUNTRY: U.
ZIP: 80203
                                                                                                                                                                                                                RESULT 12
US-08-938-105-3
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US-08-938-105-3
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                                                                                                                                                                                                                                                                                                                                                                     138 IGEDVYEKPISELD-RLEEKOK----ETYRRMLEQLLLAEKCHRRTVYELENEKHKHTD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 YMNKSDDFTNLLEQERERLKKLLEQEKAYQARKE-KENAKRLNKLRDEL-----V 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLKSFALMLVDEROMHIBQLGLQSQKVQDLTQKLREEBEKLKAVTYKSKEDRQKLLKLEV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 SLQKA----EEELQELREKI----- 383
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                                                                                                                                                                                                                                                                                                                                                 DAKKNKANRK---EEDVMASGTIKRHLKPSGESEKKTKKSVELSK--EDLIQLLSIMEGE 89
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                                                                                                                                                                                                                                                                               Query Match
6.7%; Score 409.5; DB 4; Length 1939;
Best Local Similarity 2.1.1%; Pred. No. 3.7e-15;
Matches 200; Conservative 181; Mismatches 297; Indels 269;
GENERAL INFORMATION:
APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE OF INVENTION: Graft Rejection
FILE REFERENCE: UCSF-0-90
CURRENT APPLICATION NUMBER: US/09/310,187A
CURRENT FILING DATE: 1999-05-12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-310-187A-1
                                                                                                                                                                                            LENGTH: 1939
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RVLSKANSEVAQWRTKYETDAIQRTE-ELERAKKKLAQRLQDAEE---AVEAVNAKCSSL 1363
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                                                                                  328 RQLRLKLVGLSQRIE----ELEETNK-----SLQKAEBELQELREKIAKGECGNSSLM 376
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                                     ---LKLEV-----DFEHKASRFSQEHEEMNAKLANQESHN
                                                                                                 377 AEVESLRKRVLEMEGKDE--EITKTEAQCRELKKKLQEEEHHSKELRLEVEKLQKRMSEL
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Patent No. 5686562
GENERAL INFORMATION:
APPLICANT: TOUGATLY, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS (TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 1215 HIGH STREET
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY:
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1005 EVAR--------LTQERGRAQADLALEKAARAELEMRLQNALNEQRVEFATL 1048
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1228 SSLEEEVSIINRQVLEKEGESKELKRIVMAESEKSQKLEESCACCRQRQPATVPELQNAA 1287
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PatentIn Release #1.0, Version #1.25
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                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFRENCE/DOCKET NUMBER: MTP-013
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
INFORMATION POS ESQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 amino acids
                                                  UMBER: US/08/466,390
06-JUN-1995
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 06-JUN-19
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                               AGV---SSGAPPGRNSFYM-GTCQDEPEQLDDWNRIAEL--QQRNRVCPPHLKTCYPLES 1928
                                                                                                                                                               1702 POLDLSIDSLD-LSCEEGTPLSITSKLPRTQPDGTSVPGEPASPISQRLPPKVESLESLY 1760
                                                                                                                                                                                                                                                                   1821 FYSTRSAPASQASLRATS--STQSLARLGSPDYGNSALLSLPGYRP----TTRSSARRSQ 1874
                                                                                                                                                                                                                                                                                             1020 IAVSPESQEVPMGRTILKVTPEKQTVPAPVRKYNSNANIITTEDNKI---HIHLGSQFKR 1076
                                                                                                                                                                                                                                                                                                                                               SPGPAAEGVS-----PVITVR-----PVNVTAEKEVSTGTVLRSPRNHLS----- 1116
                                                                                                                                                                                                                                                                                                                                                                 1117 SRPGASKVTSTI--TITP-----VTTSSTRGTQSVSGQDGSSQRP-----TPTR 1158
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                                                                                                                                        860 NELTMRKSWIPWMRKRENGPSTPQEKGPRPN-QGAGHPGELV-----LAPKQGQPLHIR 912
                                                                                                                                                                                           VTPDHENSTATLEITSPISEEFF-----SSTTVIPTLGNQKPRITIIPSPNVM 960
                                      LQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPVAST
                                                                                       GVQT---EAVCGDAAEEETPAVFIRKSFQEENHIMSNLRQVGLKKPMERSSVLDRYPPAA
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APPLICANT: TOUGHTLY, GARY
APPLICANT: TOUGHD, GRAHAM
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTP-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08470950 Patent No. 5698439 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: MTP-(
TELECPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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US-08-470-950-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RELKKKLQEBEHHSKELRLEVEKLQKRMSELEKLEEAFSRSKSECTQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 INLEKEKNLTKDLINELEVVKSRVKELECSESRLEKAELSLKDDLTKLKSFTVMLVDERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            624 EDNKIRELTLEIERLKKRLQQLEV-VEGDLMKTEDEYDQLEQKFRTEQDKANFLSQQLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683 IKHOMAKHKAIEKGEAVSOEAELRHRFRLEEAKSRDLOAEVOALKEKIHELMNKEDOLSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           743 LQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPVAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          803 GVQT---EAVCGDAAEEETPAVFIRKSFQEENHIMSNLROVGLKKPMERSSVLDRYPPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 SSLMAEVESLRKRVLEMEGKDEEI-----TKTEAQC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 TKERDELMGKLRSEEERSCELSCSVDLLKKRLD-GIEEVEREINRGRSCKGSEFT---CP
                                                                                                                                                                                           Query Match 6.7%; Score 407.5; DB 1; Length 2101; Best Local Similarity 20.3%; Pred. No. 5.3e-15; Matches 266; Conservative 228; Mismatches 524; Indels 292;
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRACATRRISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                  / MOLECULE TYPE: protein
US-08-470-950-4
```

1005 EVAR------LTQERGRAQADLALEKAARAELEMRLQNALNEQRVEFATL 1048 1539 1761 FTPIPARSQAPLESSLDSLGDVFLDSGRKTRSARRRTTQIINITMTKKLDVEEPDSANSS 1820 1108 QSBAAGRTEPTGPKLEALRAEVSKLEQQCQXQQEQADSLERSLEAERASRAERDSALETL 1167 1592 AAEHYKLQMEKAKTHYDAKKQQNQELQEQLRSLEQLQKENKELRAEA---ERLGHELQQA 1648 SQKPKSADPTLGPERAMSPVTITTISREKSPEGGRSAFADRPA-SPIQIMTVSTSAAPTE 1019 :|| : || : || : :::| || : :::| || : : ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || :: 1649 GLKTKEAEQTCRHLTAQ-----VRSLEAQVAHADQQLRDLG-KFQVATDALKSREPQAK 1701 EKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGS--AEPEKV 122 ------REVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLK 333 -----RELKKKLQEEEHHSKELRLEVEKLQKRMSELEKLEEAFSRSKSECTQLH 452 453 INLEKEKNLTKDLINELEVVKSRVKELECSESRLEKAELSLKDDLTKLKSFTVMLVDERK 512 860 NELTMRKSWIPWMRKRENGPSTPQEKGPRPN-QGAGHPGELV-----LAPKQGQPLHIR 912 913 VTPDHENSTATLEITSPISEEFF-----SSTIVIPTLGNQKPRITIIPSPNVM 960 LRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTVYEL : :: |: |: |: |: |: |: |-||
1487 AETRLAEVQREAQSTARELEVMTAKYEGAKVKVLEE----RQRFQEERQK---LTAQVEE ENEKHKHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQARKEKENAKRLNKLRDELVKL 243 KSFALMLVDERQMHIEQL----GLQSQKVQDLTQKLREEEEKLKAVTYKSKED----334 LVGLSQRIEELEETNKSLQKAEEELQELREK-------IAKG---ECGN---513 NAMEKIKĢEERKVDGLNKNF---KVEQGKVMDVTEKLIEESKKLLKLKSEMEE--KEYSL 568 TKERDELMGKLRSEEERSCELSCSVDLLKKRLD-GIEEVEREINRGRSCKGSEFT---CP GVQT----EAVCGDAAEEETPAVFIRKSFQEENHIMSNLRQVGLKKPMERSSVLDRYPPAA 624 EDNKIRELTLEIERLKKRLQQLEV-VEGDLMKTEDEYDQLEQKFRTEQDKANFLSQQLEE 683 IKHQMAKHKAIEKGEAVSQEAELRHRFRLEEAKSRDLQAEVQALKEKIHELMNKEDQLSQ 743 LQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPVAST SSLMAEVESLRKRVLEMEGKDEEI ------TKTEAOC-----

Search completed: September 7, 2004, 13:18:12 Job time : 45 secs us-10-788-793-2.rapb

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(without alignments)
2416.829 Million cell updates/sec
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1 MRSRNOGGESSSNGHVSCPK......KIELKKSAASSTASLGGGKG 1212
                                                                                                                                                                                                September 7, 2004, 13:16:39 ; Search time 158 Seconds
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/ Ggn2_6/ptodate/2/pubpaa/PCT_NEW_PUB.pep:*
/ Ggn2_6/ptodate/2/pubpaa/US06_NEW_PUB.pep:*
/ Ggn2_6/ptodate/2/pubpaa/US06_NEW_PUB.pep:*
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/ Ggn2_6/ptodate/2/pubpaa/US08_NEW_PUB.pep:*
/ Ggn2_6/ptodate/2/pubpaa/US08_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1298764 segs, 315065143 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ď	Sequence 111, Appl Sequence 14, Appl Sequence 12, Appl Sequence 10, Appl Sequence 3569, Ap Sequence 24, Appl Sequence 24, Appl Sequence 48, Appl Sequence 495, Appl Sequence 6, Appl Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli
Description	Sequence 2119, Apples Sequence 14, Apples Sequence 16, Apples Sequence 10, Apples Sequence 25, Apples Sequence 48, Apples Sequence 495, Apples Sequence 8, Apples Sequence 8, Apples Sequence 38, Apples Sequence 22, Apples Seque
SUMMARIES ID	US-10-408-765A-2119 US-10-309-851-14 US-10-309-851-16 US-10-309-851-16 US-10-309-851-10 US-10-309-851-10 US-10-309-851-24 US-00-925-302-495 US-00-309-851-8 US-10-309-851-8 US-10-309-851-8 US-10-309-851-8 US-10-309-851-8 US-10-309-851-8 US-10-309-851-8
	04440440444 04444 0
% Query Match Length DB	1111 11133 11135 11135 11135 764 785 7752 7752 7752 7350 839 336
% Query Match	0444 0888 0888 0888 0888 0888 0888 0888
Score	24 53 01 24 44 4 5 24 44 4 5 24 44 4 5 26 5 2 6 26 6 7 5 26 6 7 5 26 7 6 26 8 7
Result No.	11

Seguence 3353, Ap	Sequence 36, Appl	4	2	10	62,	104	104	36,	n	1586	5128,	5129,	764	107,	74	105,	105,	6564,	164	7	162	103	4	86,	106	Sequence 106, App	64,	e 2164	Sequence 5368, Ap
US-10-104-047-3353	US-10-309-851-36	-10-309-8	-10-0	-10-107-7	US-10-236-031B-62	-10 - 02	-10-107-782-10	US-10-028-248A-36	US-10-107-782-36	US-10-369-493-1586	US-10-369-493-5128	-10 - 36	US-10-032-585-7646	US-10-028-248A-107	US-10-107-782-107	-10-0	-10-107-78	US-10-369-493-6564	US-10-171-311-164	-09-927-597	US-10-171-311-162	US-10-341-434-103	US-09-927-597-4	US-10-259-194A-86	US-10-028-248A-106	-10-107-78	US-10-094-466-64	US-10-369-493-21643	US-10-369-493-5368
15	14	14	15	15	15	15	15	15	15	15	15	15	14	15	15	15	15	15	14	10	14	15	10	15	15	15	15	15	15
274	240	240	1961	1961	1960	1960	1960	1959	1959	1790	2020	2020	1881	1999	1999	1961	1961	1164	1938	1945	1972	1972	1979	1905	1959	1959	1978	880	1827
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16	17								25						31		33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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99 MLRTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETYRRMLEQLILLAEKCHRRTVYELENEKHRHTDYMNKSDDFTNLLEQERERLKKLLEQEK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ETYRRMLEQLILAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKKLLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLKTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQK 60
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                                                                         APPLICANT: Change, Sounitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Baing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
FILE REFERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.2%; Score 5301; DB 16;
94.6%; Pred. No. 3.5e-279;
tive 28; Mismatches 32;
              Sequence 2119, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1054; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-408-765A-2119
US-10-408-765A-2119
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## APPLICANT: Saus, Juan ### APPLICANT: Revert-Ros, Francisco ### TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity ### TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein ### TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein ### FILE REFERENCE: 98, 723-F-US ### CURRENT APPLICATION WUMBER: US/10/309, 851 ### CURRENT PILING DATE: 2002-12-04 ### NUMBER OF SEQ ID NOS: 38 ### SOFTWARE: PartentIn version 3.1 ### SEQ ID NO 14 ### IENGTH: 1133 ### TITLE OF INVENTION OF THE OF	Query Match         40.3%;         Score 2452.5;         DB 14;         Length 1133;           Best Local Similarity         46.2%;         Pred. No. 1.4e-124;         Indels 81;         Gaps 19;           Matches 542;         Conservative 214;         Mismatches 337;         Indels 81;         Gaps 19;           Qy         Instrangodessesnormycopressilsspockgpenakknknknkse-DWAASTIKKHLK 59         : : : : : : : : : : : : : : : : : : :	60 PSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYG   ::   ::  :  :  :	OY 176 RETVELLEBERKHINKL 235	OY 296 LKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAE 355 1     : : : :             :	Qy 416 HSKELRLEVEKLÖRRMSELEKLEBEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSR 475	Qy         536 QGKVMDVTEKLIEBSKKLIKLKSEMEEKEYSIJTKERDELMGKLRSEEERSCELSCSVDLL 595           Db         529 QNKVTYTVTEKLIEBTKRALKSKTDVEEKOMSVTKRENDLKNKLKAEEEKGNDLLSRVNML 588           Qy         596 KKRLDGIEBEVREINRGRSCREFTCPEDNKIRELTERLKKKRLQOLEVOED 551           Qy         596 KNRLDGIEBEVBEINRGR	Qy 652 LMKTEDEYDQLEQKFRTEQDKANFLSQQLEEIKHQWAKHKAIEKGEAVSQEAELRHFFRL 711	Qy 712 EBAKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYSVLQQRFMEBETKNKNMGREVLNL 771
	459 KNLTKOLLNELEVVKSRVKELECSESRLEKAELSLKODLTKLKSFTVMLVDERKNMMEKI 518	1-1 4 > E	599 VSQEABLAKHYENEBAKASHIJI	### ##################################	939 TVIPTLGNOKPRITIIPSPNVMSOKPKSADPTLGPERAMSPVTITTISREKSPEGGRSAP 998	1059 ITTEDNKIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTAEKEVSTGTVLRSPRNHLSSR 1118	1179 NLTKFOPRAETOSMKIELKKSAASSTASLGGGKG 1212 	RESULT 2 US-10-309-851-14 ; Sequence 14, Application US/10309851 ; Publication No US20030108554A1 ; GENERAL INFORMATION:

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Sequence 12, Application US/10309851
Sequence 12, Application US/10309851
Publication No. US20030108554A1
GENERAL INFORMATION:
APPLICANT: Saus, Juan
APPLICANT: Revert-Ros, Francisco
TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFERENCE: 98,723-F-US
CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSPEGGRSAFADRPASPIQIMTVSTSAAPTEIAVSPESQEVPMGRTILKVTPEKQTVPAP 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 VRKYNSNANIITTEDNKIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTAEKEVSTGTVL 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    823 INGQLYEESENQD-----EDPNDEGSVLSFKCSQSTPCPVN----RKLWIPWMKSK 869
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                                                                                                                                                                                                                                 588
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 289 TRLEKELQTQTTTKFHQDQDTIMAKLTNEDSQNRQLQQKLAALSRQIDELEETNRSLRKAE 348
                                                                                                                                                                                                                                                             KKRLDGIEEVEREINRGR----SCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGD 651
                                                                                                                                                                                                                                                                                                                                        870 EGHLQNG-----KMQTKPNANFVQPGDLVLSHTPGQPLHIKVTPDHVQNTATLEITSPTT
                                                                                                                                                            LMKTEDEYDOLEOKFRTEODKANFLSQOLEEIKHOMAKHKAIEKGEAVSQEAELRHRFRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E----NGPSTPQEKGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTS
                                                                                                                                                                                                                                                                                                                                                                              EEAKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYSVLQQRFMEBETKNKNMGREVLNL
                              BELOELREKIAKGECGNSSLMAEVESLRKRVLEMEGKDEBITKTEAQCRELKKKLQEBEH
                                                                                     HSKELRLEVEKLOKRMSELEKLEEAFSRSKSECTOLHLNLEKEKNLTKDLLNELEVVKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                       TKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP-
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Publication No. US20030108554A1
GENERAL INFORMATION:
APPLICAWT: Saus, Outen
APPLICAWT: Saus, Outen
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFERENCE: 98,723-F-US
CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
TENDER OF 10 NO 16
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                                              823 INGQLYEESENQD-----EXLWIPWMKSK 869
                                                                                                    E--EFFSSTTVIPTLGNOKPRITIIPSPNVMSQKPK-SADPTLGPERAMSPVTITTISRE 988
                                                                                                                                                            PSGESEK----KTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYG 115
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                                                                                    E----NGPSTPQEKGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTS 931
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TKELERYRHFSKSLRPSLNGRRISDPQVFSKEVQTEAV----DNEPPDYKSLIPLERAV 822
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40.2%; Score 2444.5; DB 14; Length 1133;
Best Local Similarity 46.1%; Pred. No. 3.9e-124;
Matches 541; Conservative 214; Mismatches 338; Indels 81; (
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US-10-309-851-16
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                                          ESPHSYTSTAVIPUCGTPKQRITILQNASITPVKSKTSTEDLMNLEQGMSPITWATFARA
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| Publication No. US20040005560A1
| GENERAL INFORMATION NO. US20040005560A1
| APPLICANT: HELIX RESEARCH INSTITUTE
| TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
| TILE REPERROR: HI-A0106
| CURRENT APPLICATION NUMBER: US/10/108,260A
| CURRENT PLING DATE: 2002-03-27
| NUMBER OF SEQ ID NOS: 5458
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 4080
| LENGTH: 512
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39.6%; Score 2406.5; DB 1
Best Local Similarity 94.1%; Pred. No. 1.6e-122;
Matches 482; Conservative 18; Mismatches 11;
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                                                                                                               DB 14; Length 1135;
                                                                                                             Query Match
40.2%; Score 2444.5; DB 3
Best Local Similarity 46.1%; Pred. No. 3.9e-124
Matches 541; Conservative 214; Mismatches 338
                                                         sapiens
; SEQ ID NO 12
; LENGTH: 1135
; TYPE: PRT
; ORGANISM: HOMO 8
US-10-309-851-12
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                                                                                                                                                                                                                        Sequence 3569, Application US/10108260A
| Publication No. US20040005560A1
| GENERAL INFORMATION:
| APPLICANT: HELIX RESERRCH INSTITUTE
| TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
| FILE REFERENCE: H1-A0106
| CURRENT APPLICATION NUMBER: US/10/108,260A
| CURRENT FILICE DESCRIPTION NUMBER: 2002-03-27
| NUMBER OF SEQ ID NOS: 5458
| SOFTWARE: Patentin Ver. 2.1
| ENGTH: 824
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                                                                        EEAKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYSVLQQR
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US-10-108-260A-3569
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US-10-108-260A-3569
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APPLICANT: Saus, Juan
APPLICANT: Saus, Juan
APPLICANT: Revert-Ros, Francisco
TITLE OF INVENTION: Gips, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFERENCE: 98,723-F-US
CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
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                          512
, Sequence 10, Application US/10309851
; Publication No. US20030108554A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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924 RKSFQE-ENHIMSNLRQVGLKKPMERSSVLDRYPPAANELTWRKSWIPWMRKRE- 876    1	VRPVNVTAEKEVSTGTVERS 	APPLICANT: Gannavarapu, Manjula APPLICANT: Hocrah, Sebastian TITLE OF INVENTION: NOVEL GENES, TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY TITLE OF INVENTION: OF CERVICAL CANCER TITLE OF INVENTION: OF CERVICAL CANCER FILE REFERENCE: MRI-035 CURRENT APPLICATION NUMBER: US/10/171,311 CURRENT PELING DATE: 2001-06-13 PRIOR APPLICATION NUMBER: US 60/298,155 PRIOR FILING DATE: 2001-06-13 PRIOR FILING DATE: 2001-06-13 PRIOR FILING DATE: 2001-06-13 PRIOR FILING DATE: 2001-11-14 NUMBER OF SEQ ID NOS: 238 SEQ ID NOS: 238 SEQ ID NOS: 238 LENGTH: 752 LENGTH: 752 TYPE: PRT ORGANISM: Home saniens	10-171-311-48  Query Match Best Local Simila Matches 363, Co 248 MIVDE 1 MVVDE 308 RFSQE 61 KFHQDE 368 GECGN
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QY         952 TIIPSENVMSOKEK-SADPTLGEBRAMSPVTITTISREKSPEGGRSAFADRPASPIQIMT 1010           Db         638 TILQNASITPVKSKTSTEDLMNLEQGMSPTTMATFARACTPESCGSLTPERTWSPILLS:           QY         1011 VSTSAAPTEIAVSPESQEVEMGRTILKVTPEKQTVPAPVRKTNSNANITTTEDNKIHIHL 1070           Db         698 VTGSASSPEQGRSPETTEISAKHAIFRVSPDRQSSWQFQRSNSNSSSVITTEDNKIHIHL 757           QY         1071 GSQFKRSPGPAAEGVSPVITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTTT 1130           Db         758 GSPYMQAVASPVRPASPSAPLQDNRTQGLINGALNKTTINKVTSSTTI 804           QY         1131 TPVTTSSTRGTQ 1142           Db         805 TPTATFLPRQSQ 816	RESULT 8  US-10-309-851-24  US-10-309-851-24  Sequence 24, Application US/10309851  Publication No. US20030108554A1  FURBLIANT: Saus, Juan  APPLICANT: Saus, Juan  APPLICANT: Revert Ros, Francisco  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity  TITLE OF INVENTION: GIPE, a Family of Family	Query Match         27.5%; Score 1675; DB 14; Length 785;           Best Local Similarity 45.9%; Pred. No. 1.4e-82;         1.4e-82;           Matches 373; Conservative 143; Mismatches 232; Indels 64; Gaps 14;           Qy 358 LQELREKIAKGEGONSLMAEVESLRKRVLDREGKDEFITKTEAQCRELKKKLQEEEHHS 417           LDDIKEKISKGEYGNAGIMAEVESLRKRVLDMEGKDEFITKTEAQCRELKKKLQEEEHHS 417           LDDIKEKISKGEYGNAGIMAEVESLRKRVLDMEGKDEFITKMERGKNLTKLLASFTLOS           QY 418 KELRLEVEKIQKRRMELKLERDEFRKSKGECYGLKCNLEKERMTTKQLSQELESLKVRIK 120           QY 478 BLECSESRLEKABLSKLEDLTKLKSFTVMLVDERKNNMEKIKQESRKVDGINKNFKVCG           QY 478 BLECSESRLEKABLSKLEDLTKLKSFTVMLVDERKNNMEKIKQESRKVDGINKNFFVCG           QY 538 KVMPVTEKLIEBSRKLLKKLKSEMEEKFSYLTERDELMGKLRSEEBRSCELSCSULLKK 597           LDD 181 KVTTYTEKLIEBSKKLLKKSEMEEKFSYLTERDELMGKLRSEEBRSCELSCSCYDLLKK 597           LIGH	

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                                                                                                                                                                                                                                                                                                                                                                                        124 LRPSLNGRRISDPQVFSKEVQTEAV----DNEPPDYKSLIPLERAVINGQLYEESENQD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  885 KGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTSE--EFFSSTTVIP 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 NCGTPKQRITILQNASITPVKSKTSTEDLMNLEQGMSPITMATFARAQTPESCGSLTPER 340
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  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                 665 KFRTEQDKANFLSQQLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEEAKSRDLQAEVQ 724
                                                                                                                                                                                                                                                                                                                                                      785 LRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP-----AVFIRKSFQE-ENHI 833
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12.8%; Score 780.5; DB 12; Length 439;
Best Local Similarity 41.7%; Pred. No. 2.3e-34;
Matches 186; Conservative 74; Mismatches 139; Indels 47;
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Publication No. US20030064072A9

GENERAL INPORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-05

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 1000-03-05

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 495
                                                                                                                     Indels
                                                                    Query Match 12.8%; Score 780.5; DB 9; Best Local Similarity 41.7%; Pred. No. 2.3e-34; Matches 186; Conservative 74; Mismatches 139;
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; OTHER INFORMATION: Xaa equals any of the naturally
US-09-925-302-495
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         ; OTHER INFORMAL US-09-925-302-495
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US-09-925-302-495
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                                                                      BINRGR----SCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDLMKTEDEYDQLE 663
                                                                                                                                                                                                                                                                                                                                                   347 DFLKNKLNQDSGKSTTALHQENNKIKELSQEVERLKLKLKDMKAIEDDLMKTEDEYETLE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                  784 ALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETP-----AVFIRKSFQE-ENH 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLRPSLNGRRISDPQVFSKEVQTEAV----DNEPPDYKSLIPLERAVINGQLYEESENQ 580
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (416)
121 GEYGNAGIMAEV-------EBLIKMEEQCRDLNKRLERETLQSKDFKLEVEKL 166
                                                                                                                                                                                                                                   EESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKRLDGIEEVER 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QALKEKIHELMNKEDQLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSR 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              833 IMSNIRQVGLKKPMERSSVL----DRYPPAANELIMRKSWIPWMRKRE----NGPSTPQ 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPISE--EFFSSTTVI 941
                                              QKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSRVKELECSESRLE
                                                                                                                                        KAELSLKDDLTKLKSFTVMLVDERKONMBKIKQBERKVDGLNKNFKVEQGKVMDVTEKLI
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| Patent No. US20020044941A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REPERENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT FILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: PCT/US00/05918
| PRIOR FILING DATE: 2000-06
| PRIOR FILING DATE: 1999-03
| PRIOR PLICATION NUMBER: 60/124,270
| WUMBER OF SEQ ID NOS: 896
| SOFTWARE: PatentIn Ver: 2.0
| SEQ ID NO 495
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ORGANISM: Homo sapiens
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US-09-925-302-495
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Sequence 6, Application US/10309851
Publication No. US2030108554A1
Publication No. US2030108554A1
PUBLICANT: Saus, Juan
APPLICANT: Saus, Juan
TITLE OF INVENTION: GIPB, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFERENCE: 98,723 F-703
CURRENT FILIS DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3:1
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APPLICANT: Saus, Juan
APPLICANT: Saus, Juan
APPLICANT: Revert-Ros, Francisco
TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Alteract with Goodpasture Antigen Binding Protein
FILE REFREENCE: 98, 72.3-F-03
CURRENT APLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Version 3.1
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    289 TRLEKELQTQTTKFHQDQDTIMAKLTNEDSQNRQLQQKLAALSRQIDELEETNRSLRKAE 348
                                                                                296 LKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETINKSLQKAE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 REDVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDR 152
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Publication No. US20030108554A1
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Matches 138; Conservative
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; ORGANISM: Homo sapiens
US-10-309-851-6
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LENGTH: 265
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US-10-309-851-6
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PUDICation No. US2030108554A1
GENERAL INFORMATION:
APPLICANT: Saus, Juan
APPLICANT: Revert-Ros Francisco
TITLE OF INVENTION: GIPE, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFERENCE: 98,723-F-US
CURRENT PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1002 PASPIQIMTVSTSAAPTEIAVSPESQEVPMGRTILKVTPEKQTVPAPVRKYNSNANIITT 1061
                                                                                                                                                                                                                                                                                                                                                                                                943 TLGNOKPRITIIPSPNVMSQKPK-SADPTLGPERAMSPVTITTISREKSPEGGRSAFADR 1001
                                                                                                       64 ALKEKIHEYMATEDLICHLQGDHSVLQKKLNQQENRNRDLGREIENLTKELERYRHFSKS 123
                                                                                                                                                       785 I.R.P.S.GNGRRMVDVPVASTGVQTEAVCGDAAEETP-----AVFIRKSFQE-ENHI 833
                                                                                                                                                                                     179 ------BDPNDEGSVLSFKCSQSTPCPVN----RKLWIPWMKSKEGHLQNG-----K 220
                                                                                                                                                                                                                                                                                                                  885 KGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTSE--EFFSSTTVIP 942
                                                                                                                                                                                                                                                                                                                                         221 MQTKPNANFVQPGDLVLSHTPGQPLHIKVTPDHVQNTATLEITSPTTESPHSYTSTAVIP 280
                                                                                                                                                                                                                                                                                                                                                                                                                            281 NCGTPKQRITILQNASITPVKSKTSTEDLANNLEQGMSPITMATFARAQTPESCGSLIPER 340
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                                                                           725 ALKEKIHELMNKEDQLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSRA 784
                                                                                                                                                                                                                                      834 MSNLRQVGLKKPMERSSVL----DRYPPAANELTMRKSWIPWMRKRE----NGPSTPQE 884
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                       60 PSGESEK----KTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 SAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCH 175
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46.4%; Pred. No. 6.9e-34;
ive 71; Mismatches 106; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1062 EDNKIHIHLGSQFKRSPGPAAEGVSP 1087
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SEQ ID NO 8
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Best Local Similarity 46.4%
Matches 168; Conservative
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ORGANISM: Homo sapiens
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1033 RTILKVTPEKQTVPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSPGPAAEGVSPVITVR 1092
                                                                                                  973 PERAMSPVTITTISREKSPEGGRSAFADRPASPIQIMTVSTSAAPTEIAVSPESQEVPMG 1032
                                                         160 DHVQNTATLEITSPTTESPHSYTSTAVIPNCGTPKQRITILQNASITPVKSKTSTEDLMN 219
                                                                                                                          220 LEQGMSPITWATFARAQTPESCGSLTPERTMSPIQVLAVTGSASSPEQGRSPETEISAK 279
                                                                                                                                                                                                  DHENSTATLEITSPISE--EFFSSITVIPTLGNOKPRITIIPSPNVMSOKPK-SADPTLG
                                                                                                                                                                                                                                                           1093 PVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTRGTQ 1142
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Publication No. US20030108554A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: GIPS, a Family of Polypeptides with Transcription Factor Activity TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein File Reference: 98,723-F-US CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Version 3.1
SEQ ID NO 22
                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                            58 NEPPDYKSLIPLERAVINGQLYEESENQD-----EDPNDEGSVLSFKCSQSTPCPV 108
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                                                                                                                                                                                                  3 QQENRNRDLGREIENLTKELERYRHFSKSLRPSLNGRRISDPQVFSKEVQTEAV----D
                                                                                                                                                                            756 EEETKNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAAE
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                                                                                                  DB 14; Length 384;
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                                                                                            10.2%; Score 618.5; DB 14; Length 37.8%; Pred. No. 1.2e-25; Live 70; Mismatches 126; Indels
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                                                                                                                  Best Local Similarity 37.8
Matches 155; Conservative
                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-851-38
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LENGTH: 384
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Compugen Ltd.
GenCore version
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OM protein - protein search, using sw model

3; Search time 51 Seconds (without alignments) 2285.963 Million cell updates/sec September 7, 2004, 13:08:23 Run on:

US-10-788-793-2 6082 1 MRSRNQGGESSSNGHVSCPK......KIELKKSAASSTASLGGGKG 1212 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	H		01000000000000000000000000000000000000		SUMMARIES	Deac		4 tor	8296 myos	myosin	31 myosin	S28261 centromere protein	33	hypothetica	liver stage a	myosin heav	hypothetical	myosin heavy	A43336 microtubule-vesicl	smooth			Donwoou		restin		A41604 myosin heavy chain	conserv	myosin heavy	T13030 microtubule bindin	hypothetical	4922 myosin heavy	T13829 Tpr homolog - frui	S28589 trichohyalin - rab	
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myosin heavy chain	embryonic muscle m	myosin heavy chain	citron - mouse	nuclear/mitotic ap	early endosome ant	myosin heavy chain	slow myosin heavy	myosin heavy chain	trichohyalin - hum	myosin heavy chain	myosin heavy chain	plectin - rat	myosin II heavy ch	myosin heavy chain	hypothetical prote
S2434B	A59236	JX0178	S68420	T30336	A57013	A26655	A59234	138055	A45973	S04090	A36014	A39638	S61477	A29320	T16416
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7.1		7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	

# ALIGNMENTS

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tpr protein - human N/Alternate names: kinase-related transforming protein (tpr-met); protein with promoter

C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence revision 26-May-1995 #text\_change 11-Jan-2002
C; Accession: S33124; S33740; S00928; G01185
C; Accession: S33124; S33740; S00928; G01185
Oncogene 7, 2329-2333, 1992
A; Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive coi A; Reference number: S33124; MUID:93064711; PMID:1437155

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A, Molecule type: mRNA A, Residues: 1-204 < MTT> A, Notes references: EMEL:X66397; NID:g633225 A, Notes the nucleotide sequence was submitted to the EMBL Data Library, October 1991 R; Mitchell, P.J.; Cooper, C.S. Oncogene 7, 383-388, 1992 A; Title: Nucleotide sequence analysis of human tpr cDNA clones. A; Reference number: \$23740; MUID:92195670; PMID:1549355

A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID:g37258
R;King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
Oncogene 2, 617-619, 1988
A;Rifle: Tpr honologues activate met and raf.
A;Reference number: S00928; MUID:88262257; PMID:3387099
A;Accession: S00928

A;Molecule type: mRNA A;Residues: 1-31,'R',33-142 <KIN> A;Cross-references: EMBL:Y00672; NID:g37255; PIDN:CAA68681.1; PID:g37256

submitted to the EMBL Data Library, December 1995 A;Reference number: H00592

A; Accession: G01185

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DMA A;Residues: 144-228 <GRE> A;Cross-references: EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; PID:g1296798

A;Cross-references: GDB:128821; OMIM:189940 A;Map position: 1q25-1q25 A;Introns: 177/3

67; Gaps Query Match 7.8%; Score 476; DB 2; Length 2094; Best Local Similarity 20.4%; Pred. No. 1.1e-08; Matches 314; Conservative 252; Mismatches 510; Indels 460;

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F;1-211,222-631,653-2007/Product: myosin heav F;88-802/Domain: myosin motor domain homology F;178-185/Region: nucleotide-binding motif A F;212-221/Region: alternatively spliced segme F;559-593/Region: alternatively spliced segme F;632-652/Region: actin binding #status predi F;692-714/Region: actin binding #status predi	F;875-2007/Domain: coiled coil #status predic F;875-1115/Region: 132 F;1316-2007/Region: 11ght meromyosin F;129/Modified site: N6,N6,N6-trimethyllysine F;129/Modified site: N6,N6,N8-trimethyllysine F;124/Alinding site: ATP (Lys) #status predict F;735,742/Active site: Cys #status predicted F;735,48inding site: Dosephate (Thr) (covalen	Query Match Best Local Similarity 20.6%; Pred. No. 1 Matches 259; Conservative 250; Mismatch	Qy 67 KTKKSVELSKEDLIQLLSIMEGELQAREDVI	Db   914 QQLLEEKNILAEQLQAETE!!!   1   1   1   1   1   1   1   1   1	Qy 237 DELVKLKSFALMLVDERQMHIEQLGLQSQKV :   :     :     :     :     :     :     :       :       :	DD 1069 DLEERLKKEEKTRĢELEKARRLDGETTDLO QY 322NQESHNRQLRLKLVGLSQRIEELE DD 1129 RGDEBAVQRNNALKVIRELQAQIAELQEDLE	375 1182 433		OY	Qy         645 LEVVEGDLMKTEDEYDQLEQKFRTEQDKANF
Db 1061 DEENKONKDLTNELQOTQLKLGETEKSLAAQVAATKKASDERDTLSQNL 1108  Qy 312 EHEEMNAKLANQESHNRQLRLKLVGLSQRIEELE-ETNKSLQKAEBELQELREKIAK 367	1167	Qy       473 KSRVKELECSESRLEKAELSLKDDLTKLKSFTVMLV 508          :: : :          :          :                    :: : :         :          :                           Db       1287 KAKAKDLEAQLNEVQDNHEKAVADAELLNKKKAQSDKELNSLKAELEALTKAKSV       1341         Qy       509 DERKON	DD 1342 VESKOKDSENEKAALSEEIDQANEKLKNIQADLRKATADLQEANEKKAEVEAQRDKLVAD 1401  QY 550 SKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKRL 599  :     :	QY 600 DG-IEBVEREINRGRSCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDL 652	Db 1522 QSAEEBLNELRSKADKDKKKISELEEQVNELESRPVGTGNADENEIKIRDAQIADLNKAL 1581  Qy 710 RLEEAKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYSVLQQRFWEEE 758  1582 EMKGVQNNQLQATNKELKAKDNDLTSKIEITENEMKKLENAKKRLEQDKDEADKAVSEQT 1641	QY 759 TKNKNMGREVLALIKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAA 814  DD 1642 IKRKGLEEEVKKLTTEIQALKFQINAPSSVAQEEEKQRLESDIAELKEQLEQERTTAA 1699  QY 815 EEETPAVFIRKSFQEE-NHIMSNLRQV 840	_	1-Dec-1993 #text_change 19-Apr-2002 , R.S.	onmuscie myosin spe gangari	A;Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide set A;Accession: A43402 A;Accession: A43402 A;Molecule type: mRNA A;Residues: 1-211;222-631;653-2007 <ta2> A;Cross-references: GB:M93676; NID:9212448; PIDN:AA448985.1; PID:9212449 A;Note: sequence extracted from NCBI backbone (NCBIN:112864) C;Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle myc C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated F;1-2007/Froduct: myosin heavy chain-B, neuronal #status predicted <myn></myn></ta2>

avy chain-B, nonmuscle #status predicted <MYS SGARQKLQLEKVTA-----EAKIKKME 1015 CRELKKKLQEE-EHHSKELRLEVEKLQKRMS 432 : |:| |::|:: LESDNKELACEVKVLQQVKAESEHKRKKLDA 1290 :| |: ::: |:| |: ---NELDNVSSLLEEAEKKGIKFAKDAAS 1343 ||:::||:::| EEEKNNLQEQQEEBEARKNLEKQMLALQAQ 1403 | | : | : | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 | : 15 - FDQMLAEEKNISARYAEERDRAEAEAREK 1512 :: : | :| ||||| | : XIAECTSQLAEEEEKAKNLAKLKNKQEMMIT 1068 ||::| | |:: NDMEDLMSSKDDVGKNVHELEKSK-RTLEQQ 1571 SRERLKKLLEQEKAYQARKEKENAKRLNKLR 236 CVODLTOKLREEEKLKAVT----- 285 ----LEVDFEHKASRFSQEHEEMNAKLA 321 JEETNKSLOKAEBELQELREKIAKGECGNSS 374 --NLTKOLLNELEVVK------S 474 IVMLVDERKNMMEKIKQEERKVDGLNKNFKV 534 SEKEYSLTKERDELMGKLRSEEERSCELSCS 591 SCKGSEFTCPEDNKIRELTLEIERLKKRLQQ 644 VFLSQQLEEIKHQMAKH------ 690 ----RLEEAKSRDLQAE 722 /IHMLRTEKTKPEVLEAHYGSAEPEKVLR-- 124 SV-----LQQRFMEEETKNKNMGREVLN 770 .5; DB 1; Length 2007; 1.4e-08; ches 456; Indels 295; Gaps gy <MMOT> A (P-loop) ment 1 #status experimental dicted ment 2 #status experimental dicted icted <COI> ne (Lys) #status predicted sted ent) #status predicted ent) #status predicted

Db 1	572 VEEMRTQLEELEDELQATEDAKLRLEVNMQAMKAQFERDLQARDEQNEEKKRMLVKQVRE 1631	Cigenetics: content of the content o
oy od o	771 LTKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETPAVFIR-KSFQE 829 	
Oy Db	830 ENHIMSNLRQVGLK-KPMERSSVLDRYPPAANELTWRKSWIPWMRKRENGPS 880	C.Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide F;84-764/Domain: myosin mctor domain homology <mmot> F:174-181/Region: nucleotide-binding motif A (P-loop) F;552-565/Region: actin binding #status predicted</mmot>
oy D	881 TPQEKGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTSEEFSSTTV 940	F;626-640/Region: actin binding #status predicted F;837-1938/Domain: coiled coil #status predicted <coi> F;837-127/Domain: S2 #status predicted <ds2> F;1278-1961/Domain: light meromyosin #status predicted <lmm></lmm></ds2></coi>
Oy Db	941 IPTLGNQKPRITIIPSPNVMSQKPKSADPTLGPERAMSPVTITTISREKSPEGG-RSAFA 999 197 UDTLNSELAGERSAAQKSENARQQLERQNKELKAKLQELEGSVKSKF- 1843	Fi1939-1961/Domain: carboxyl-terminal <cbt> Fi125/Modified site: NG.NG.Nertrimethyllyaine (Lys) #status predicted Fi180/Binding site: ATP (Lyg) #status predicted Fi894,704/Active site: Cys #status predicted</cbt>
Oy 1	1000 DRPASPIQIMTVSTSAAPTEIAVSPESQEVPMGRTILKVTPEK-CTVPAPVRKYNSNANI 1058 	Query Match 7.7%; Score 469.5; DB 1; Length 1961; Best Local Similarity 22.9%; Pred. No. 1.6e-08; Matches 228; Conservative 181; Mismatches 341; Indels 247; Gaps 40;
Oy 1	1059 ITTEDNKIHIHLGSQFKRSPQPAAEGVSPVITVREVNVTAEKEVSTGTVLRSPRNHLSSR 1118 :	Qy 67 KTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVI 126
Oy 1	1119 PCASKVTSTITITPVITSSTRGTQSVSGQDGSSQRPTP 1156	QY 127 HRDAILAQEKSIGEDVYEKPISEL-DRLEEKQKETYRRMLEQLLLAEKCH-RRTVYELEN 184  1
RESULT 4 A61211 Myosin heavy chain NyAlternate names: N;Contains: myosin C;Species: Home sa; C;Date: 12-May-1996 C;Accession: A6123 R;Simons M: Wang Circ. Res. 69, 530 A;Title: Human non A;Reference number: A;Accession: A6123 A;Molecule type: M A;Accession: A4187 A;Cross references R;Sacz, CG; Myerin A;Reference number: A;Accession: A4887 A;Accession: A4887 A;Accession: A15-19 A;Cross references R;Tochtaker, L.E; B;Accession: A15-19 A;Reference number: A;Accession: A15-19 A;Reference number: A;Accession: A15-19 A;Reference number: A;Referen	RESULT 4  A01211  MyOsin heavy chain nonmuscle form A - human Nathernate names: cellular myosin heavy chain; myosin type 9; NWMHC-A Nathernate names: cellular myosin heavy chain; myosin type 9; NWMHC-A Nathernate names: cellular myosin heavy chain; myosin type 9; NWMHC-A C) Edec: 12.04.13 C) Edec: 12.04 C) Edec: 12.04.13 C) Edec: 12.04 C) E	0.00   0.00

QY 327 NRQLRLKLVGL-SQRIEELBETNKSLQKABEELQELREKIAKGECGNSSLMAEVES 381	QY 382 LRRRVLEMEGKDEEITKTEAQCRELKKLQEEEHHSKELRLEVEKLQKRMSELEKL 437	QY 438EBAPSRSKSECTQLHINLEKEKNITKDLINELEVVKSRVKELECSESRLEKA 489 :::::	QY 490 ELSLKDDLTKLKSFTVMLVDERKNNMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLIEE 549	QY 550 SKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKRLDGIEEVEREI 609	QY 610 NRGRSCKGSEFTCPEDNKIRELTILEIERLKKRLQQLEVVEGDLMKTEDEYDQLEQKFRTE 669	QY 670 QDKANFLSQQLEEIKHQMAKHKAI	Qy 708 RFRLEEAKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYSVLQ 751	QY 752 QRFMEEETKNKNMGREVLALIKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCG 811	QY 812 DAAEEETPAVFIRKSFQEENHIMSNLRQVGLKKPMERSSVL 852   :    :      :      :    :    :    :	QY 853DRYPPAANELTMRKSWIPWMRKRENGPSTPQEKGPRPNGGAGHPGEL 899 :	QY 900 VLAPKQGQPLHIRVTPDHENSTATLEITSPTSEEFFSSTTVIPTLGNQKPRITIIPSPNV 959	QY 960 MSQKPKSADPTLGPERAMSPVTITISREKSPEGGRSAFADRPASP 1005  1:   :	QY 1006 IQIMTVSTSAAPTEIAVSPESQEV-PMGRTILKVTPEKQTVPAPVRKYNSNANIITTEDN 1064	QY 1065 KIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTA 1098	QY 1099 EKEVSPGASKVT 1125	QY 1126 STITITPVTISSTRGTQSVSGQDGSSQRPTPTRIPMSKGMKAGKPV 1171	RESULT 6 S67593 transport protein USO1 - yeast (Saccharomyces cerevisiae)
1481 SLARALEEAMEQKAELERLNKQFRTEMEDLMSSKDDVGKSVHELEKSKRALEQQVE 1536 725 ALKEKIHELMNKEDQLSQLQVDYSVLQQRFWEEETKNKNMGREVLNLT 772	1537 EMKTQLEELEDELQATEDAKLRLEVNLQAMKAQFERDLGGRDEGSEEKKKQLVRCVREME 1596 773 KELELSKRYSRALRPSGNGRRWVDVPVASTGVQTEAVCDDAAEBETPAVFIRKSFQEE 830	1597 AELE-DERKQRSMAVAARKKLEMDLKDLEAHIDSANKNDBAIKQLRKLQAQMK 1649 831NHIMSNLRQVGLK-KPMERSSVLDRYPPAANELTMRKSWIPWMRKRE 976	1650 DCMRELDDTRASREEILAGAKENEKKLKSMEAEMIOLOEELAAAERAKROA 1700 877 NGFSTPOEKGPRPNQGAGHPGELVLAPKOGOPLHIRV 913	1701QQERDELADEIANSSGKGALALEEKRRLEARI 1732	RESULT 5 258261 Centromere protein E - human N/Alternate names: centromere 312K protein; kinesin-related protein CENP-E	C.Species: Homo saplens (man) C.bate. 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001 C.Accession: S28261 R.Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.	Nature 359, 536-539, 1992 Affitels CENP-E is a putative kinetochore motor that accumulates just before mitosis. A;Reference number: \$28261; MUID:93024922; PMID:1406971	A;Molecule type: mRNA A;Residues: 1-2663 <yen> A;Cross references: EMBL:Z15005; NID:g29864; PIDN:CAA78727.1; PID:g29865 C;Genetics:</yen>	A;Gene: GDB:CENPE A;Cross-references: GDB:361164; OMIM:117143 A;Map position: 4Q24-4Q25 C;Superfamily: centromere protein B; kinesin motor domain homology C;Keywords: ATP; coiled coil; microtubule binding: mitosis; nucleotide binding: P-loop	<pre>kinesin motor domain homology <kmot> nucleotide-binding motif A (P-loop) n: coiled coil #status predicted <coi></coi></kmot></pre>	Length 2663;	MACCHES 2/9; CONSELVATIVE 26/; MISMACCHES 455; INDELS 3/6; GAPS 62;  33 SEDAKKNRANRKEEDVMASGTIKRHLKPSGESEKKTKKSVE 73  1382 SACKORGALWAKEKUNE-TEVIVEWENGEKEKRENGELETETEMIGISKEINEWEGVA 1441	LSKEDLIQLLSIMEGEL-QAREDVIHMLRTE-KTKPEVLEAHYGSAEPEKVLRVLHRDAI	LAQEKSIGEDVYEKPISEL-DRLEEKQKETYRRMLEQLLLAEKCHR	NLSEKETEISTIOKOLEAINDKLONKIQEIYEKE-EQLNIKQISEVOENVNELKOFKEHR RTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQARKEKENAK : : : : : : : : : : : : : : : : : : :	231 RL-NKLRDELVKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKL 274  1615 BIVARKESQERYQFLKATAVNETQERACEIEHLKEQFFQKKLALENIETENIELTOLL 1674	275 REEEEKLKAVTYKSKEDRQKLLKLEVDFEHKASRFSQEHEEMNAKLANQESH 326 

Qy         438EEAFSRSKSECTQLHLNIEKEKNLTKD	QY   634 EIERLKKELQQLEVVEGDLMKT-EDEYDQLEGKFRTEQDKANFLSQQLEEIKHQMAKHKA 692   1	RESULT 7 T21174 hypothetical protein F20G4.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000 C;Accession: T21174; T25113 R;McMursay, A. submitted to the EMBL Data Library, June 1996 A;Reference number: Z19385 A;Accession: T21174 A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Retaus: preliminary; translated From A;References: EMBL:Z75538; PIDN:CAA98841.1; GSPDB:GN00019; CESP:F20G4.3	SPDB:GN00019; CESP:F20G4	Query Match  Query Match  Best Local Similarity 20.7%; Pred. No. 2.78-08;  Matches 268; Conservative 233; Mismatches 443; Indels 351; Gaps 52;  Qy 55 KRHLKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKP 107;  Db 885 EQELKVTAEKLRRSEVFISDYKQQMEKMDEERLVLKTRLDAESSERAEIFEERSRWAARR 944  Qy 108 EVLEAHYGSAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQ 167
C;Species: Saccharomyces cerevisiae C;Sate: 12-Jul-1996 #sequence_revisiae C;Jate: 12-Jul-1996 #sequence_revisiae C;Jate: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000 C;Accession: S67593, A3455; 530782 R;Bloceker, H.; Brandt, P. Submitted to the Protein Sequence Database, July 1996 A;Reference number: S67587 A;Accession: S67593 A;Accession:	A,Accession: A38455 A,Moclecule type: DNA A,Residues: 1-389, TA',392-724,'S',726-1790 <nak> A,Residues: 1-389, TA',392-724,'S',726-1790 <nak> A,Residues: 1-389, TA',392-724,'S',726-1790 <nak> A,Residues: 1-389, TA',392-724,'S',726-1790 <nak> A,Residues: 1-389, TA', 392-724,'S',726-1790 <nak> A,Residues: Translated the codon ACT for residue 768 as 11e R,Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E. submitted to the EMBL inbrary, February 1993 A,Residues: DAN A,Residues: 330782 A,Moclecule type: DNA A,Residues: 71-846,'E',848-923,'K',925-1252,'I',1254-1318,'V',1320-1460,'S',1462-1580,'S A,Generics: EMBL:L03188 C,Generics: A,Gene: SGD:S0002216; MIPS:YDL058W A,Gene: A,Adences SGD:S0002216; MIPS:YDL058W A,Map Dostiton: 41.</nak></nak></nak></nak></nak>	Circywords: coiled coil; transmembrane protein Circywords: coiled coil; transmembrane #status predicted <tm1> E;326-342/Domain: transmembrane #status predicted <tm2> E;344-410/Domain: transmembrane #status predicted <tm2> E;344-410/Domain: transmembrane #status predicted <tm3> Cuery Match  Query Match  Query Match  Query Match  At EDAKKNRANREEDVMASGTIKRHLKPSGESEKKTKKSVELSKEDLIQLISIMEG 88  34 EDAKKNRANREEDVMASGTIKRHLKPSGESEKKTKKSVELSKEDLIQLISIMEG 88  BB EKDKSNVHHQKETKSLKEDJAAKITEIKAINENLEEMKIQCNNLSKEKEHISKELVETKS 948  Qy  BB ELQAREDVIHMIRTEKTKERDLAAKITEIKAINENLEEMKIQCNNLSKEKEHISKELVETKS 948  Qy  BB ELQAREDVIHMIRTEKTKERDLAAKITEIKAINENLEEMKIQCNNLSKEKEHISKELVETKS 148  CONTRACTOR OF STATUS 148  CONTRACTOR OF STATUS 148  CONTRACTOR OF STATUS 148  CONTRACTOR OF STATUS 148  CONTRACTOR OF STATUS 148</tm3></tm2></tm2></tm1>	Db 949 RPÖSHDINIVAKL-TEKLKSLANNYKDMOATENESLITAVEESKNESSIQLSNLÖNKID 1004  Qy 149 ELDRIEEKOKETYRRMLEQLILABKCHRRTVYELBEREKHKHTDYMKSDDFTNLLEQ 205  1005 SMQGKENPQIERGSIEKNIEQLKTTISDLEQTKEEIIRKSDSSKDEYES 1054  Oy 206 ERRIKKLIROEKAYOAKEKEN-AKRINKLRDELVKLKSFALMINDEROWHEQLGLGS 264  1055 QISLLKEKL-ETATTANDENVNKISELTKTREELBAELAAYKNLKNELETKLETSEKAL 1112  Oy 265 QKVQDLTQKLREEEKLKAVTYKSKEDRQKLLKLEVDFEHKASRPSGEHEEMNAKLANGE 324  1113 KEVKENEEHLKEEKIQLEKEATETKQQINSLRANLESLEKEHEDLAAQLKKYE 1165  Oy 325SHNRQLRLKGOSRIEBLEETHKAQNASLRANLESLEKEHEDLAAQLKKYE 1165  Oy 325SHNRQLRLKJOERE-ESTUKSLQARBEELQ	Db 1166 EQIANKERÇYNEEISQLADEİTSTQQENESİKKKODELEGEVKAMKSTSEEQSNLKKSEI 1225  Qy 360ELREKIAKGECGNSSLWAEVESLEKRKVLENEGKDEEITKTEAQCRELKKKLQ-EE 413  1226 DALNLQİKELKKKNETNEASİLESİKSVESETVKİKELQDECNFKEKEVSELEDKİKASE 1285  Qy 414 EHHSK

අු	ò	qa 	ò	අු	RESULT	A45592 liver a	C;Speci C;Date:	C; Acces R; Zhu,	A;Refer	A; Molec	A; kesid A; Cross B: Zhu	Mol. Bi	A; Refer	A; Molec	A; Note:	Nature	A; Litte A; Refer A; Acces	A;Statu b:Molec	A; Resid	R, Gueri	A; Descr	A; Refer A; Acces	A; Scatu A; Molec	A; Kesid A; Cross	A; Note: C; Comme	C;Super C;Keywo	1-101/4	Query Best Match		Š 1	9 6	ò 1	3 8	7 A	è
::     :    :  :: :   :  :: :   :   :	DEDECTI DESTONATOR DE LE EQUANCADO ES NAL I EMVRIL DE PLA EN EN EN EN EN EN EN EN SE	168 LALAEKCHRKIVYELENEKHKHIDYMNKSDDFINLLEQEREKLKKLL 214			CREEEE	1115 KESELSQISIRNDEELAARQQLEREIRRIRAQLDDAIEETNKEKAARQKAEKARRDMAEE 1174	VAKLANQESH-NRQLRLKLVGLSQRIEELEETN-KS	1175 LESYKQELEESNDKTVLHSQLKAKRDEEYAHLQKQLEETVKSSEEVVEEMKAQNQKKIEE 1234	354 AEBELQEL-REKIAKGECGNSSLMAEVESLRKRVLEMEGKDEBITKTEAQCREL 406	KRQKISADKAKSSAESDNENFRAELS	407 KKKLQEEBHHSKELRLEVEKLQKRMSELEKLEBAFSRSKSECTQLHLNLEKEKNLTKDL- 465	IKMREMQSNLDDLMAKLSKMNNELESIQ	SLEVVKSRVKEL 	1344 LSELTEASEEDRRTRATLNNKIRQLEEDLAVAVEARDDALDAQEKIEK 1391	VDGLNKNFKVEQGKVMDVTEKLIEESKKLLKLKLKSEMEEKEYSLTKERD	1392 EVKEVKSLLAEARKKLDEENREVMEELRKKKEKELSAEKERADMAEQARD 1441	581 BEERSCELSCSVDLLKKRLDGIEEVEREINRGRSCKGSEFTCPEDNKIRELTLEIER-LK 639 :   :   :   :   :   :   :  :	KKKAIQEAEDVQKELTDVVAATREMERK	640 KRLQQLBVVBGDLMKTEDEYDQLEQKFRTEQDKANFLSQQLBEIKHQMAKHKAIEKG 696	1477 KFDQQLAEBRNNTLLAQQBRDMAHQMLRDAETKALVLSNBLSBKKDIVDQLBKDKRTLKL 1536	697 EAVSQEAELRHRFRLEEAKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYS 748	1537 BIDNLASTKDDAGKNVYELEKTKRR-LDEELSRAEQQIIELEDALQLADDARSRVEVNMQ 1595	749 VLQORF MEEETKNKNMGREVLNLTKELELSKR780	::	WPVASTGVQTEAVCGDAAE	1656 EKNEASLRQIEDLSRQLRKAQLGWKDLQLDVTEARAAME-DALAGQRDAEKRARASEDEI 1714	FOEENHIMSNLRQVGLKKPMERSSV	1715 KRLTADIQAVSSSKRKAEAERDELIEEVSSLRASSFSNEEKRRLEAKVIDLEDQLDEEAS 1774	859 ANELTMRKSWIPWMRKRENGPSTPQEKGPRPNQGAGHPGELVLAPKQGQPLHIRVTPDHE 918	1775 ANELAQEKVRKSQE 1791	919 NSTATLEITSPTSEEFFSSTTVIPTLGNOKPRITIIPSPNVMSOKPKSADPTLGPERAMS 978	1792 QMTADLAMERSVCERTESDKIALERANRDLKQQLQDAEN 1830	979 PVTITTISREKSPEGGRSAFADRPASPIQIMTVSTSAAPTEIAVSPESQE-VPMGRTI 1035	ilrtilnvaeakvssleoo	1036LKVTPEKQTVPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSFGP 1080
£	3 ,	કે ર્દ	6	q	ò	q	ò	q	ò	g	à	q	ò	q	ò	g	ò	QQ	ò	g	ò	g	ò	g	ò	ą	ò	QQ	ò	g	ò	qq	ઠે	අ	à

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se-references: EMBL:M28266
Fin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Pataxapotikul, J.; Beaudoin, ted to the EMBL Data Library, April 1992
Fription: a liver-stage-sepcific antigen of plasmodium falciparum characterized by stence number: $34842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ecule type: DNA
idues: 323-381,'HKAI' <GUE2>
ser-references: EMBL:M28266
e: difference at carboxyl end due to frameshift error
nent: This protein is found as flocculent material in the parasitophorous vacuole.
Arfamily: trichohyalin; calmodulin repeat homology
1871 METKWAEMQQMLEEEKRQGESNRQAVDRQNARIRQLRTQLEDTEAERDRLTNKLKDERRR 1930
                                                                                          1931 AEE------MIDLNETLSRDVSLLKQRETTARRIPGLIGHRESRRFGSN------TSL 1976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 HKHTDYMNKSDDFTNLLEQERERLKKL-----LEQEKAYQARKEKENAKRLNKLRDELV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                       stage antigen LSA-1 - malaria parasite (Plasmodium falciparum)
sies: Plasmodium falciparum
s: 22-Nov-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jun-2000
ssion: S24597; A45592; $29393; S34842; B45592; C45592; D45592
7. J.; Hollingdale, M.
                                                       1081 AAEGVSPVITVRPVNVTAEKEVS-----TGTVLRSPR--NHLSSRPGASKVTSTITITPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQQSDLEQERLAKEKLQEQQRD--LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 EDAKKNKANRKEEDVMASGTIKRHLKPSG---ESEKKTKKSVE-----LSKEDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 7.6%; Score 462.5; DB 2; Length 1909;
Local Similarity 24.8%; Pred. No. 2.7e-08;
hes 239; Conservative 188; Mismatches 340; Indels 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iochem. Parasicol. 48, 223-226, 1991
e: Structure of Plasmodium falciparum liver stage antigen-1.
rence number: A45592; MUID:92107224; PMID:1840628
                                                                                                                                                                1134 TISSIRGIQSVSGQDGSSQRPIPTRIPMSKGMKAG 1168
                                                                                                                                                                                                   1977 ARDEFRGS-ALTNEMSPSDRPA-SRLTSGTGSQLG 2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dues: 1-1909 <ZHU>
Is-references: EMBL:X56203; NID:g9915; PID:g9916
J.; Hollingdale, M.R.
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cule type: DNA
dues: 323-387 <GUE1>
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Biochem. Biophys. Res. Commun. 175, 244-249, 1991 A;Title: A unique cellular myosin II exhibiting differential expression in the cerebral of A;Reference number: PN0013; MUID:91151356; PMID:1998509 A;Accession: PN0013 A;Molecule type: mRNA A;Residues: 1914-1998, I' <su2> A;Residues: 1914-1998, I' <su2> C;Superfamily: myosin heavy chain; myosin motor domain homology C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide F;84-763/Domain: myosin motor domain homology <mmot></mmot></su2></su2>	F:174-181/Region: nucleotide-binding motif A (P-loop) F:514-575/Region: actin binding #status predicted F:551-575/Region: actin binding #status predicted F:653-675/Region: actin binding #status predicted F:836-1959/Domanin: colled coil #status predicted <coi>F:836-1276/Region: S: F:127-1959/Region: 1ight meromyosin F:125/Modified site: NG.NG.crimethyllysine (Lys) #status predicted F:180/Bindding site: ATP (Lys) #status predicted</coi>	F:693,703/Active site: Cys #status predicted F:1916/Binding site: phosphate (Ser) (covalent) #status predicted F:1943/Binding site: phosphate (Ser) (covalent) #status predicted Custy Match Query Match Best Local Similarity 24.3%; Pred. No. 3.18-08; Matches 210; Conservative 160; Mismatches 260; Indels 235; Gaps 40;	Qy 67 KTXKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEK-TKPEVLEAHYGSAEPEKVLR- 124	OY 176 RRTUYELENEKHKITDYMNKSDDFTWLLEGERERLKKLLEGEKAYQARKEKENAKRLAKL  DD 929 RNQILQNEKKKEQGHKNDLEEQLDEMESARQKLQLEKUTTEAK-LKKL 975  OY 236 RDELVKLKSFALMLVDERQWHIEQLGLQSQKVQDLTQKLREEEERLKAVTYKSKEDRQKL 295  DD 976 EEEQIILEDQNCKLAKEKKLLEDHARFTWLTREEERSKSKSLA-KLKNKHEAN 1027	Qy         296         LKLEVDFEHKASRFSOEHEEWNAKLANOESHNRQLRLKLVGLSQRIEELEETNKSL         351           bb         1028         1TDLEBERLRREEKQRQELEKTRRKLEGDSTDLSDQIABLQAQIABLKWQL         1077           Qy         352         QKAEBELQELRERKIAKGECGNSSLMARVESERRKKLEMEG         391           Db         1078         AKKEBELQAALARVEBEAAQKNWALKKIRELESQISELQEDLESERASRNKAEKQKRDLG         1137	392 KDEBITKTEAQCRELKKKLQEBEHHSKELRLEVEKLQKRMSE ::	Db 1197 VEELABQUEGTKRKVA
	QY         355 EBELQEL-REKIAKGECGNSSLMAEVESLRKRVLEMEGKDEETTKTEAQ 402           1145 GEQOSDLEQERLAKEKLGEOGSDLEOFRRAKEKLGEOGSDLERTKASKETLGEOGSDLEQ 1204           QY         403 CRELKKKLCAGERHSENERLEVEKTKORNSELEKLEBAFSRSKSECT 449           Db         1205 ERLAKEKLQEOGSDLEOFRRAKEKLQEOGSDLEOFRLAKEKLQEOGSDLEOFRRAKEKLQ 1264	QY         450 QLHLMLEKEKNLTKDLLNELEVVKSRVKELECSESRLEKAELSLKDDLTKLKSFTVM 506           Db         1265 EQQSDLEQERRAKEKLQEQQSDLEQERRAKEKLQEQSDLEQERLA-KEKLQEQSS 1319           QY         507 LVDERKNMMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLIEESKKLLKLKSEMEEK 563           Db         1320DLEGERLAKEKLDEGOSD	564 ENSITEMBELMOKIRSEERSCELSCOVDLIKKIL-DGIEBEVREININGRSCKGSEFT  1369 QSDLEQERRAKEKLQEQQSDLEQDRLAKEKLQEQQRDLEQERRAK 622 CPEDNKIRELTLEIERIKKRLQQLEVVEGDLMKIEDEYDQLEQKEKTEQDKAN  11   1   1   1   1   1   1   1   1   1	675 FLEQOLEEIVHOWARGHAILERGEAVSOBELENHERLEEAKSRDLOBEUGEKRA	1521CREDILEGERIAMERINGEGGRULEGERKAAKKINGECOSDILEGERRAKEKINGEGGGSDI. 792RRWYDVPVASTGVOTEAVCGDAAEEETPAVFIRKSFOEERHIMSNILRGVGLK. 1577 EQERRAKEKIQEGGSDILEGERIAKEKIQEGGRDILEGERLAKEKIQEGGRDILEG-RKADTK 844 KPMERSSVILDRYPPAANELTMRKEWIPWMRKEENGFSTPOEKGFR	1682	RESULT 9 SRESULT 9 SRESULT 9 STATE 12 MyOsin heavy chain, neuronal (similarity) - rat MyAlternate names: myosin II NyContains: myosin AfPase (EC 3.6.4.1) NyContains: myosin AfPase (EC 3.6.4.1) NyContains: myosin AfPase (EC 3.6.4.1) C.Speciase: Rattus norregicus (Norway rat) C.Speciases: Rattus norregicus (Norway rat) C.Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 19-Apr-2002 C.Accession: S21801; PN0013; S18134 NyColor E. Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain A.Reference number: S21801; MUID: 92235856; PMID: 1569576 A.Accession: S21801 A.Molecule type: mRNA A.Residues: 1-1999 &SUN> A.Residues: 1-1999 &SUN> A.Cross-references: EMBL.X62659 R.Sun, W.; Chantler, P.D.

	Oy   585 SCELSCSVDLLKKRLDGIEEVEREINRGRSCKGSEFTCPE 624	44; 81 257 127	:::   A;Residues: 1-1938 < NYI>   KQLQISYDA 317   A;Residues: 1-1938 < NYI>   KQLQISYDA 317   A;Residues: 1-1938 < NYI>   KQLQISYDA 317   A;Cross-references: GB:X55714; NID:g5611; PIDN:CDA39247.1; PID:g5612   C;Keywords: actin binding; myosin motor domain homology contraction; nucleotide coil; hydrolase; muscle contraction; nucleotide binding motif A (P-loop)   F;87-586/Region: nucleotide-binding motif A (P-loop)   F;547-586/Region: actin binding #status predicted   F;653-675/Region: actin binding #status predicted   F;836-1938/Domain: colled coil #status predicted   F;836-1938/Domain: colled coil #status predicted   F;127-1938/Region: 11ght meromyosin   F;127-1938/Region: 11ght meromyosin   F;127-1938/Region: 11ght meromyosin   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active site: Cys #status predicted   F;693,703/Active   F;693,7	Value   Valu
675 FLSQQLEEIKHQMAKHKAIEKGEAVSQEAE-LRHRFRLEEAKSR	RESULT 10 124806 hypothetical protein T10G3.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caecasion: T24806 R;Burton, J. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19937 A;Accession: T24806 A;Reference number: Z19937 A;Accession: T24806 A;Reference number: Z19937 A;Rolecule Fype: DNA A;Reference number: Z19937 A;Rolecule Fype: DNA A;Reperimental Source: Clone T10G3.6 A;Experimental source: Clone T10G3.6 A;Genetics: A;Genetics: A;Genetics:	1001: 5 15/3; 73/3; 387/3; 412/3; 708/3; 818/3; 894/3; 982/3; 1080/2 15/3; 73/3; 387/3; 412/3; 708/3; 818/3; 894/3; 982/3; 1080/2 1 Similarity 23.5%; Pred. No. 2.4e-08; Indels 234; Gaps 222; Conservative 183; Mismatches 304; Indels 234; Gaps 26 SDGKGPSEDAKGNKANRKEEDVMASGTIKRHLKPSGSEKKTKKSVELSKEDLIQ 26 SPGKGPSEDAKGNKANRKEEDVMASGTIKRHLKPSGSEKKTKKSVELSKEDLIQ 27 ILISIMEGLKRELKVVKSDVVRXEIEVSRLEKGLDGRPSEDDVNVLRTELVM 82 LLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEPE-KVLRVLH	AQKLMDAISQEKDIEIKEHLANSIRNLSMEREKQHIVNENLEKKIGGEGEETVKQLQISYDA 317RDAILAQEKSIGEDVYEKPISELDRLEEKKIGGEGEETVKQLQISYDA 317  S.:.	248 MLVDERQWHIEQL

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qq	1275 SRLQAENSDLTRQLEDAEHRVSVLSKEKSQLSSQLEDARRSLEBETRARSKLQNEV 1330	qa	ğ
ò	519 KQEERKVDGLNKNFKVEQGKVMDVTEKLIEBSKKLLKLKSEMEEKEYSLTKERDEL 574	ò	ñ
qa	1331 RNWHADMDAIREQLEEEQESKSDVQRQLSKANNEIQQWRSKFESEGANRTEELEDQKRKL 1390	qq	7.
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qa	1450 TAEWQAKVNSLQSELENSQKESRGYSAELYRIKASIEEYQDSIGALRRENKNLADEHHDL 1509	qq	8
δλ	677 SQQLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEEBAKSRDLQAEVQALKEKI 730	ò	4
ą a	1510 TDQLSEGGRSTHELDKARRRLEMEKEELQAALEEAEGALEQEEAKVMRAQLEIATVRNEI 1569	qq	9
ò	731 HE-LMNKEDQLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELS-KRYSRAL 785	ò	4
qa	1570 DKRIQEKEEBFDNTRRNHQRALESMQASLEAEAKGKADAMRIKKKLEQDINELEVAL 1626	ପ୍ର	96
ò	786 RPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETPAVFIRKSFQEENHIM 834	ò	5
qq	1627 DAŠNRGKAEMEKTVKRYQQQIREMQTSIEBEQRQRDEARESYNMAERRCTLMSGEVEELR 1686	da 1	101
ò	835 SNLRQVGLKKPMERSSVLDRYPPAANELTWRKSWIPWMRKRENGPSTPQEKGPREN 890	ò	28
QQ	1687 AALEQAERARKASDNELADA-NDRVNELTSQVSSVQGQKRKLEGDINAMQTDLDEMHGEL 1745	Db 1	106
ò	891 QGAGHPGELVLAPKQGQPLHIRVTPDHEN 919	ò	64
QQ	1746 KGADERCKKAMADAARLADELRAEQDHSN 1774	Db 1	111
RESULT	12	'n	69
A43336	bule-vesicle linker CLIP-170 - human	Db 1	117
C;Speci C;Date:	ies: Homo sapiens (man)	ζō	75
C, Acces R; Pierz		Db 1	123
Cell 70 A;Title	), 887-900, 1992 3: CLIP-170 links endocytic vesicles to microfubules	PECITIE 13	
A;Refer A;Accer	rence number: A43336; MUID:92405160; PMID:1356075 ssion: A43336	JC5421 smooth muscl	ຼິ
A;Statu A;Molec A:Resid	A;Status: proliminary A;Molecule type: mRNA A:Residnes: 1-1392 <ptps< td=""><td></td><td>77</td></ptps<>		77
A, Cross	3-references: GB:M97501; NID:g180621; PIDN:AAA35693.1; PID:g180622	C;Accession R;Hasegawa Biochem. B	3, T
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80 IQLLSIMEGELQAREDVIHMLRTEKTKPEV--LEAHYGSAEP--EKVLRVLHRDAILAQE 135
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                                                                                                                                                                                                                  30 KGPSEDA---KKNKANRKEED----VMASGTIKRHL---KPSGESEKKTKKSVELSKEDL 79
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Mus musculus (house mouse)
Jun-1997 #sequence_revision 18-Jul-1997 #text_change 02-Feb-2001
tch
al Similarity 22.9%; Pred. No. 4.80-08; Indels 181; Gaps
202; Conservative 183; Mismarches 316; Indels 181; Gaps
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K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Ophys. Res. Commun. 232, 313-316, 1997
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A;Title: Molecular cloning and expression of murine smooth muscle myosin heavy chains. A;Reference number: JC5420, MUID:97242182; PMID:9125171
A;Accession: JC5421
A;Molecule type: mRNA
A;Residues: 1-1938 <HAS>
A;Cross-references: DDBJ:DB5224; NID:91945079; PIDN:BAA19691.1; PID:91945080
A;Experimental source: smooth muscle
C;Comment: This protein plays a role in smooth muscle cell contraction.
C;Comment: This protein plays a role in smooth mostle cell contraction.
C;Comment: This protein heavy chain; myosin motor domain homology
C;Reywords: nucleotide binding; P-loop
F;88-771/Domain: myosin mctor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|:|| : : : | :: | | |:: || || |:: || LEEEEAARQKLQLGLEKVTAEAKIKKLEDDI------LVMDDQNSKLSKERKLLEERVSDL 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDLDSERAARNKAEKOKRDLGEELEALKTELEDTLDSTATQOELRAKREOEVTVLKKALD 1184
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                                                                                                                                                                                                                                                                                                                                                  101 RTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKET 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEMNAKLANQESHNRQLRLKL-----AGLSQRIEELEETNKSLQK------AE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EELQELREKIAKGECGNSSLMAEVESLRKRV---LEMEGKDEEI-TKTEAQCRELKKKLQ 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DELMGKLRSEEERSCELSCSVDLLKKRL-----DGIEEVEREINRGRSCKGSEF 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 DQLEQKFRTEQDKANFLSQQLE---EIKHQMAKHKAIEKGE---AVSQEAELRHRFRLEE 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      714 AKSRDLQAEVQALKEKIHE----LMNKEDQLSQLQVDYSV------LQQRFMEEETKN 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKRQQQLTAMKVIQRNCAAYLKLRNWQWWRLFTKVKPLLQVTRQEEEMQAKEEEMQKITE
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                                                                                                                                                                                                                                                                                                                                                                                                                161 YRRMLEQLLLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERER------LKKL
                                                                                                                                                                                                                  Query Match 7.4%; Score 449; DB 2; Length 1938; Best Local Similarity 23.5%; Pred. No. 7.8e-08; Matches 203; Conservative 167; Mismatches 292; Indels 202;
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C;Species Mus musculus (f) outse mouse)
C;Species Mus musculus (f) outse mouse)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 02-Feb-2001
C;Accession: JC5420
R;Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Biochem. Biophys. Res. Commun. 232, 313-316, 1997
A;Title: Molecular cloning and expression of murine smooth muscle myosin heavy chains. A;Accession: JC5420; MUID:97242182; PMID:9125171
A;Accession: JC5420
A;Molecule type: mRNA
A;Residues: 1-1972 cHAS>
A;Cross-references: DDBJ:DB5923; NID:g1945077; PIDN:BAA19690.1; PID:g1945078
A;Experimental source: smooth muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Comment: This protein plays a role in smooth muscle cell cont C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: nucleotide binding; P-loop F;88-771/Domain: myosin motor domain homology <MMOT> F;178-185/Region: nucleotide-binding motif A (P-loop)
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us-10-788-793-2.rpr

	Db 1337 ELIQEETROKLINGSSRIRQUEERANNIQUEQUEEREARKSLEKQLISLQSQLIEAKKKUD 1396  QY 601GIEEVEREINRGRSCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDLM 653    1397 DEVGTIEGLEEVKKKLLKDTEGLGORLEEKIIAYEKLEKTKRRLQQLEUDELM 1448  QY 654 KTEDEYDQLEGKFRTEQDKANFLSQQLEEIKHQMAKH	
QY   G21 TCPEDNKI	RESULT 15 A47297 myosin heavy chain form B, nonmuscle - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Species: Xenopus laevis (African clawed frog) C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Peb-2001 C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Peb-2001 C; Accession: A47297, A65441 R; Bhatia-Dey, N; Adelstein, R.S.; Dawid, IS-Nov-1994 #text_change 02-Peb-2001 R; Bhatia-Dey, N; Adelstein, R.S.; Dawid, IS-Nov-1994 #text_change 02-Peb-2001 R; Bhatia-Dey, N; Adelstein, R.S.; Dawid, IS-Nov-1994 #text_change 02-Peb-2001 R; Reference number: A47297; MUID:931933; PMID:8464900 A; Reference number: A47297; MUID:931933; PMID:8464900 A; Reference number: A7297 A; Relley, C.A.; Oberman, F; Yisrseli, U.K.; Adelstein, R.S. J; Biol. Chem. 270, 1395-1401, 1395 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reture: preliminary A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reture: preliminary A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:7836406 A; Reference number: A55441; MUID:95138137; PMID:780406	Query Match  Query Match  Query Match  Best Local Similarity 23.1%; Pred. No. 8e-08;  Matches 198; Conservative 181; Mismatches 329; Indels 150; Gaps 32;  Qy 40 KANRKEEDVMASGTIKRHIKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQARE 94  Best Local Similarity 23.1%; Pred. No. 8e-08;  A1 KANRKEEDVMASGTIKRHIKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQARE 94  Best Local Similarity 23.1%; Pred. No. 8e-08;  A2 KANRKEEDVMASGTIKRHIKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQARE 94  Best Local Similarity 23.1%; Pred. No. 8e-08;  A2 VARGEELVAKDEELLKYKEKQSKVEGELVDMECKHQCLVEEKNILAECHAET 916  A3 DVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDR 152  BD 917 ELFAEAEEMRARLAIKKQEMEEILRDLEIRMBEEERRNQVLQN 959  CY 153 LEEKQKETYRRMLEQLLLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQGRERL- 210  BD 960 -EKKKMQYDLEGOLDEERAACKLQLEKVTAEARLIKKWHEEDLIVLEDQNHIEQLGQQK 266  CHIMIC H.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 7, 2004, 13:00:13; Search time 29 Seconds (without alignments) 2176.173 Million cell updates/sec Run on:

1 MRSRNQGGESSSNGHVSCPK......KIELKKSAASSTASLGGGKG 1212 US-10-788-793-2 6082 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SUMMARIES	Description	HUMAN P12270 homo sapien	9 homo	1 homo	5 sacch	062812	AEQIR P24733 aequipecten	P35749	8 mus mus	-	Р30622 hото в	P35748	pyrococ	K P10587	Q15075 homo 88	P12847	P37709	Q27991	P49454 homo 88	042184	Q9jlt0 rattus	P35580	P29616	Q9vje5	P13538	P49025 mus mu		Q91vw5	P1353	007283	Q9ji55 crice	P11055	_
WO'S	Ω	TPR HU	MYH9 H	CENE	USOI	MYH9_R	MYS AE		MYHB M	MXH9_C	REST_H		RASO P	MYHB_C	EEA1 H	MYH3_RAT	TRHY_RABIT	MYHA B	CENF_HUMAN	REST C	MYHA RAT	MYHA_H	MYSCC	C190_D	MYSS_CHICK	CTRO	MYS2_D	GOA4 M	MYH8_H	TRHY HUMAN	PLE1 C	MYH3 H	MYSN D
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de	Query Match	7.8	7.7	•		•	7.5	7.4	7.4	٠		•	٠	7.3	•	٠	٠	•	•						•		7.1		٠	•	7.0	7.0	7.0
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or RAF genes.
-1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/TPRID282.html".

								Q96yr5 sulfolobus				Q28641 oryctolagus
	MYHD HUMAN	MYH3_CHICK	GOA4 HUMAN	MYH2 HUMAN	GOB1 HUMAN	RASO AQUAE	AKA9 HUMAN	RASO_SULTO	MYSD_CAEEL	PLE1 HUMAN	MYH7 PIG	MYH4_RABIT
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•	1938	1940	2230	1941	3259	978	3911	879	1938	4684	1935	1938
	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.8
	426.5	426	425.5	425	422	420	420	417	417	414	413	413
	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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1556 --AIVAAKSKIAHLAGVKDQLTKENEELKQRNGALDQQKDELDVRITALKSQYEGRISRL 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 KPKSADPTLGPERAMSPVTITTISREKSPEGGRSAFADRPASPIQIMTVSTSAAPTEIAV 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1083 EGVSPVITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTI------- 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1703 PATVTNPTTTPTATVMPTTQVESQEAMQSEG------PVEHVPVFGSTSGSVRST 1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1752 SPNVQP-SISQPILTVQQQTQ-----ATAFVQPTQQSHPQIEPANQ-----ELS 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1795 SNIVEVVQSSPVERPSTSTAVFGTVSATPSSSLPKRTREEEEDSTIEASDQVSDDTVEMP 1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1129 -----TITPV-TTSSTRGTQSVSGQDGSSQRPTPTRIPMSKGMKAGKPVVAASGAGNLT 1181
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                                                             505 VMLVDERKNMMEKIKQEERK-VDG-LNKNFKVE---QGKVMDV-----TEKLIEESK--- 551
                                                                                                                                                                                                                                                                                                                                                                               646 ---EVVEGDLMKTEDEYD----QLEQKFRTEQDKANFLSQ------QLEEIKHQMA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                         689 K------HKAIEKGEAVSQEAELRHRFRLEEAKSRDLQAEVQ----ALKEKIHEL 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 MNKEDQLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSRALRPSGNGRR 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794 MVDVPVASTGVQTEAVCGDAAEBETPAVFIRKSFQEENHIMSNLRQVGLKKPME-RSSVL 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         913 VTP------DHENSTATLEITSPTSEEFFSSTTVIPTLGNOK-PRITIIPSPNVMSQ 962
                                                                                                                                                                     578 --LRSEEER-----KKRLDGIEEVER
                                                                                                                                                                                                                                                                                                  608 EINRGRSCKGSEFTCPEDNKIRELTLEIERLKKRLOOL-------------
                                                                                                                                          552 -----KLLKLKSEMBEKEYSLTKER-----DELMGK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.8%; Score 476; DB 1; Length 2349;
Best Local Similarity 20.4%; Pred. No. 1.4e-08;
Matches 314; Conservative 252; Mismatches 510; Indels 460; Gaps
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EMBL; Y00672; CAA68681.1;
Genew; HGNC:12017; TPR.
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A BADLINES FROM H. A. R. Collina J. E. Bruskiewich R., Beare D.M.,
RA Dunham I., Hunt A. R., Collina J. E., Batcs K. N., Beare D.M.,
RA Dunham I., Hunt A. R., Collina J. E., Batcs K. N., Beabley O. P.,
RA Bagguley C., Balley J., Barlow K.F., Batcs K. N., Beasley O. P.,
RA Glogo S. M., Cobley V. B., Cols C.G., Collier R. B., Connor R.,
Concy D., Corby W. E., Collier G. J., Durbin R. M., Ellington A.G.,
RA Dhami P.D., Dockree C., Doddworth S.J., Durbin R. M., Ellington A.G.,
RA Shoms K.L., Fewy J. M., Femich L., Garner A.A.,
RA HILL R. E., Hall-Tamlyn G., Heathcott R. W., Ho S., Holmes S.,
RA HILL R. E., Jangford C. F., Leversha M.A., Lloyd C., Holyd D. M.,
RAIDER E., Goward M. E., Cerethaw J., Kimberley A.M., King A.,
Laird G.K., Langford C. F., Leversha M.A., Lloyd C., Holyd D. M.,
RAIDER E., Hall-Tamlyn G., Heathcott R. W., Ho S., Mortinore B.J.,
RACISTY J. Mclaren S., McWurray A.A., Milne S. A., Mortinore B.J.,
RACISTY J. Mclaren S., McWurray A.W., Pearson D., Phillipore B.J.,
RACISTY J. Mclaren S., McWurray A.W., Pearson D., Phillipore B.J.,
RACISTY J. Mclaren S., McWurray A.W., Pearson D., Phillipore B.J.,
RACISTY J. Mclaren S., McWurray A.W., Pearson D., Phillipore B.J.,
RACISTY J. Mclaren S., McWurray A.W., Pearson D., Phillipore B.J.,
RACISTY J. Mclaren S.A., Williams D., Williams E., Willing L.,
Williams E., Williams S.A., Williamson H., Willer T. E., Wilming L.,
Williams E., Manasawi K., Sasaki T., Aaskawa S., Kodoh J.,
RADORMAN A., Fang Y., Weltzeki Y., Aoki N. M., Williams D.,
Rang M., Anna A., Pang Z., Williamson H., Willer N., Minra N.,
Rang M., Anna S., Kawasaki K., Sasaki T., Aaskawa S., Robe B.A., Don T.,
Robert M., Du., Craben P., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Williams D., Willia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M., Arnaout M.A., Clayton L.K., Tenen D.G.;
"Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, characterization of the protein, chromosomal localization, and upregulation during myeloid differentiation.";
Blood 78:1826-1833 (1991).
                                             Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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MEDLINE=90138958; PubMed=1967836;
Saez C.G., Myers J.C., Shows T.B., Leinwand L.A.;
"Human nonmuscle myosin heavy chain mRNA: generation of diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-1337 FROM N.A.
MEDLINE=92003925; PubMed=1912569;
               Homo Bapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                              SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain subunite (MHC), 2 alkali light chain subunite (MLC) and 2 chain subunite (MHC), 2 alkali light chain subunite (MLC) and 2 regulatory light chain subunites (MLC).

chain subunite (MHC), 2 alkali light chain subunite (MLC) and 2 regulatory light chain subunites (MLC).

chain subunite (MHC) is highly regetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.

Characteristic for alpha-helical coiled coils.

(MHA) [MIM:155100]. MHA is an autosomal dominant macrothrombocytopenia characterized by thrombocytopenia, glant platelets and leukocyte inclusions.

Characterized by thrombocytopenia glant platelets and leukocyte inclusions. With additional alport-like clinical features of sensoriheural deafness, cataracts and nephritis.

Characterized by thrombocytopenia alport-like clinical features of sensoriheural deafness, cataracts and nephritis.

Characterized by thrombocytopenia, glant platelets and leukocyte characterized by thrombocytopenia, and nephritis.

Characterized by thrombocytopenia, giant platelets and leukocyte characterized by thrombocytopenia, and nephritis.
                                                                                                                                                                                                                                                                                                        MEDLINE=20428192; PubMed=10973259;
Seri M., Cusano M., Gangarosas S., Caridi G., Bordo D., Lo Nigro C.,
Ghiggeri G.M., Ravazzolo R., Savino M., Del Vecchio M., d'Apolito M.,
Iolascon A., Zelante L.L., Savoia A., Balduini C.L., Noris P.,
Magrini U., Belletti S., Heath K.E., Babcock M., Glucksman M.J.,
Aliprandis E., Bizzaro N., Desnick R.J., Martignetti J.A.,
"Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and
                                                                                            MEDLINE=20489856; PubMed=11023810;
Lalwani A.K., Goldstein J.A., Kelley M.J., Luxford W., Castelein C.M.,
                                                                                                                                                               "Human nonsyndromic hereditary deafness DFNA17 is due to a mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: Cellular myosin appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- DISEASE: Defects in MYH9 are the cause of autosomal dominant nonsyndromic sensorineural deafness 17 (DFNA17) [MIM:603622]. DFNA17 is characterized by progressive hearing impairment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS MHA ILE-1155 AND LYS-1841.
MEDLINE=20428193; PubMed=10973260;
Kelley M.J., Jawien W., Ortel T.L., Korczak J.F.;
"Mutation of MYH9, encoding non-muscle myosin heavy chain A, in May-Hegglin anomaly.";
Nat. Genet. 26:106-108(2000).
                                                                                                                                                                                                                                                              VARIANTS MHA/FTNS/SBS LYS-93; CYS-702; CYS-1165; HIS-1424 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
                   Proc. Natl. Acad. Sci. U.S.A. 87:1164-1168(1990).
through alternative polyadenylylation.";
                                                                                                                                                                                                              J. Hum. Genet. 67:1121-1128(2000).
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Nat. Genet. 26:103-105(2000).
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EMBL, M69180; AAA61765.1; -.
EMBL, M31013; AAA36349.1; -.
                                                                VARIANT DFNA17 HIS-705.
                                                                                                                                                                                          nonmuscle myosin MYH9
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PIR; A61231; A61231. HSSP; P10587; 1BR2. Genew; HGNC:7579; MYH9.

us-10-788-793-2.rsp

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                                                                                       KTE-----AQCRELK-----KKLQEEEHHSKELRLEVEKLQKRMSELEKLEE
                                                                                                                      687 MAKHKAIEKGEAVSQEAELRH---RFRLE--------EAKSRDLQAEVQA
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MEDLINE-95196755; PubMed-7889940;
Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
"Mitotic Hela calls contain a CENP-E-associated minus end-directed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Centromeric protein E (CENP-E protein).
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MIM; 160775; -..

R MIM; 155400; -..

R MIM; 605249; -..

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R MIM; 603249; -..

R MIM; FRO00049; MYOSIN, Lail.

R PEAN; PRO017; SPCCTIN.

R PROD17; SPCCTIN.

R PROSITE; PSCO96; IQ; 1.

R PROSITE; PSCO96; IQ; 1.

R MYOSIN, APP-binding; Calmodulin-binding; Actin-binding; Coiled coil; MILigene family; Dieses mutation; Deafness.

T DOMAIN 779 MULL GOTTON MACSIN HEAD-LIKE.

T DOMAIN 837 1926 COLLED COIL (POTENTIAL).

T DOMAIN 654 676 ACTIN BINDING.

T WARIANT 93 93 N. -> K (IN MHA).
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ATP (POTENTIAL).
ACTIN-BINDING.
N -> K (IN MIA).
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/FTIGHVAR 010797.

EAI -> RGH (IN REF. 3).

T -> S (IN REF. 3).

T -> M (IN REF. 4).

C -> Y (IN REF. 4).

KG -> GR (IN REF. 4).

KG -> GR (IN REF. 4).
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/FTId=VAR 010791.
R -> C (IN FTNS).
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/FTId=VAR 010794.
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                                                                                                                                                      reveals
                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 275:30451-30457 (2000).
- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 IOF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION.
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                                                                                                                        Chan G.K.T., Schaar B.T., Yen T.J.;
"Characterization of the kinetochore binding domain of CENP-E relateractions with the kinetochore proteins CENP-F and hBUBR1.";
J. Cell Biol. 143:49-63(1998).
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267; Mismatches 455; Indels 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: INTERACTS WITH CENP-F AND BUBRI KINASE.
BUCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE,
QUANTITATIVELY DISCARDED AT THE BND OF THE CELL DIVISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2663;
                                                                                                                                                                                                                                                          MEDLINE=20459117; PubMed=10852915;
Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong
Bishop W.R., Kirschmeier P.;
                                                                                                                                                                                                                                                                                                                                              farnesylation of
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GO; GO:0008350; F:kinetochore motor activity; TAS.
GO; GO:0000067; P:DNA replication and chromosome cycle; TAS.
GO; GO:0007079; P:mitotic chromosome movement; TAS.
GO; GO:0007089; P:mitotic metaphase plate congression; TAS.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin, 1.
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312087 MW; CEFC13880C8C8CBB CRC64;
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ATP (BY SIMILARITY).
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2.6e-08;
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GO; GO:0005699; C:kinetochore; TAS.
                                                                    CHARACTERIZATION.
MEDLINE=98437347; Pubmed=9763420;
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  microtubule motor.";
EMBO J. 14:918-926(1995).
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J. Biol. Chem ?
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                              ----NVTA 1098
                                                                                                                                                                                                                        2515 EKEISKLKQQNEQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPKSPKVT 2574
                                                                                                                                                                                                                                                                                                                                  STIT----ITPVTTSSTRGTQSVSGQDGSSQRPTPTRIP------MSKGMKAGKPV 1171
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required for protein transport from the ER to the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complex.
SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE ER AND THE GOLGI COMPLEX.
DOMAIN: The rodlike tail sequence is highly repetitive, composed of an heptapeptide repeat pattern characteristic of alpha-helical coiled coils. May form filamentous structures in the cell.
SIMILARITY: BELONGS TO THE VDP/USOI/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A cytoskeleton-related gene, usol, is required for intracellular protein transport in Saccharomyces cerevisiae."; J. Cell Biol. 113:245-260(1991).
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01-MAY-1992 (Rel. 22, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
115-MAR-2004 (Rel. 43, Last annotation update)
116-MAR-2004 (Rel. 43, Last annotation update)
116-MAR-2004 (Rel. 43, Last annotation update)
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MEDLINE=91185402; PubMed=2010462;
Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,
Yamasaki M.;
                              KIHIHL-----GSQFKRSPGPAAEGVSPVITVRPV--
                                                                                                                                                           EKEVS-----TGTVLRSPRNHLSSR----
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EMBL; L03188; AAB00143.1; --
EMBL; U53668; AAB00143.1; --
GETMOININE; 140300; --
SOU02214; SOU02214; USOL,
INTERPO; IPR002918; ARM.
INTERPO; IPR002917; Spectrin.
INTERPO; IPR005953; USOL_BILS_C.
INTERPO; IPR006953; USOL_BILS_C.
PÉAM; PF04871; USOL_P115_C; 1.
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                                                                  stack; Cytoskeleton; Coiled coil
                                                                                                                                                               COLLED COIL (POTENTIAL).
CHARGED (HYPER-HYDROPHILIC).
DISPENSABLE FOR THE PROTEIN FUNCTION.
ASP/GLU-RICH (ACIDIC).
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206424 MW; 6CE2B216E9FD4818 CRC64;
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                                               1675 LDEKAMLLETKYNDLVNKEQAWKRDEDTVKKTTDSQRQEIEKLAKELDNLKAENSKLKEA 1734
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Subunit: Myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2).

DOWAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.

SIMILARITY: Contains I myosin-like globular head domain.
                   IEKGEAVSQEAELRHRFRLEEAKSRDLQAEVQALKEKIHELMNKED----QLSQLQVDYSV
                                                                                                           LOORFMEERTK----NKNMG------REVLNLTKELELSKRYSRALRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choi O.H., Park C., Itoh K., Adelstein R.S., Beaven M.A.;
Submitted (JuL-1995) to the EMBL/Genbank/DBU databases.
-!- PUNCTION: Cellular myosin appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and
                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain,
type A) (Nonmuscle myosin heavy chain-A) (NWMHC-A).
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SMART; SM00242; MYSc; 1.
PROSITE; PSS0096; IQ; 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQ.
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ATP (POTENTIAL).
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InterPro; IPR001609; myosin_head.
InterPro; IPR00409; Myosin_head.
InterPro; IPR00409; Myosin_N.
InterPro; IPR005028; Myosin_tail.
Pfam; PF00161; IQ; I.
Pfam; PF00163; myosin_head; I.
Pfam; PF001576; Myosin_hil.
Pfam; PR00193; Myosin_tail; I.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD0000355; myosin_head; I.
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                                                                                                                                                                                                                                                                                                    125 VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTVYELEN
                                                                                                                                                                                                      841 IRHEDELLAKBAELTK-VREKHLAAENRLTEMETMQSQLMAEKLQLQEQLQAKTELCAEA
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                                                                       Length 1961;
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676 ACTIN-BINDING.
226336 MW; 9B9B76D9681FB19E CRC64;
                                                                    7.5%; Score 458.5; DB 1;
llarity 23.5%; Pred. No. 4.2e-08;
Conservative 163; Mismatches 283;
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01-MAR-1992 (Rel. 21, Last sequence update)
15-MAR-2004 (Rel. 31, Last annotation update)
Myosin heavy chain, striated muscle.
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X: MEDINES-8441913; PubMed=8805510;
X: Houdusse A., Cohen C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.; Ander C.
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                                                                                                  TISSUE-Adductor muscle, MEDLINSSUE-SAdductor muscle, MEDLINE-22011955; PubMed-1917970, MEDLINE-22011955; PubMed-1917970, MEDLINE-22011955; PubMed-1917970, Cooplete primary structure of a scallop striated muscle myosin heachain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation."; J. Baol. Chem. 266:18469-18476(1991).
Eukaryota; Metazoa; Mollugca; Bivalvia; Pteriomorphia; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
NCBL_TaxID=31199;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94173332; PubMed=8127365; Xie X., Harrison D.H., Schlichting I., Sweet R.M., Kalabokis V.N., Szent-Gyorgyi A.G., Cohen C.; Structure of the regulatory domain of scallop myosin at 2.8-A resolution.";
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSERE-Adductor muscle;
MEDIATSERE-Adductor muscle;
MEDIATORIAN DE PubMed=2263488;
Nyitray L., Goodwin E.B., Szent-Gyorgyi A.G.;
"Nucleotide sequence of full length cDNA for a scallop striated muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158 (1990).
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PDB, 1SCM, 30-APR-94.
PDB, 1MCM, 30-APR-94.
PDB, 1MCM, 11-UUL-96.
PDB, 1KCM, 09-OCT-02.
PDB, 1KCM, 20-NOV-02.
PDB, 1LCO, 20-NOV-02.
PDB, 1LCO, 20-NOV-02.
PDB, 1LCO, 1PR001609; Myosin head.
InterPro, 1PR001609; Myosin head.
InterPro, 1PR001609; Myosin, head.
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InterPro, 1PR001909; Myosin, head.
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Pfam; PP0013; myosin_head; 1.
Pfam; PP01736; Myosin_h; 1.
Pfam; PP01756; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD0000355; myosin_head; 1.
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                                                                                SEQUENCE FROM N.A.
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64 SEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEPEKVL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 LREEBEKLKAVTYKSKEDROKLLKLEVDFEHKASRFSOEHEEMNAKLANOESHNROLRLK 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 --LLLAEKCH-RRTVYELENEKHK-HTDYMNKSDDFTNL---LEQERERLKKLLEQEKAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 SRV------KELECSESRL----EKABLS--LKDDLTKLKSFTVMLVDERKNWMEKI
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                                                                                                                                                                                                                                                                                                                                                                                                                            7.5%; Score 457; DB 1; Length 1938;
llarity 22.6%; Pred. No. 4.7-e-08; Onservative 205; Mismatches 382; Indels 178; Gaps
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSS; 1.
PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Calmodulin-binding; 3D-structure.
ATP-binding; Calmodulin-binding; MYOSIN HEAD-LIKE.
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DASNRGKAEMEKTVKRYQQQIREMQTSIEEEQRQRDEARESYNMAERRCTLMSGEVEELR 1686
                               RPSGNGRRMVDVPVASTGVQTEAVCGDAAEETPAVFIRKSFQ------EENHIM 834
                                                                          SNLRQVGLKKPMERSSVLDRYPPAANELTMRKSWIPWMRKRENGP----STPQEKGPRPN 890
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,

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Puhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,

Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,

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MEDLINE=93263189; PubMed=7684189;
Matsuoka R., Yoshida M.C., Furutani Y., Imamura S., Kanda N.,
Yanagisawa M., Masaki T., Takao A.;
"Human smooth muscle myosin heavy chain gene mapped to chromosomal region 16q12.";
                                                                                                                                                                                                                                                                                     Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Kikuno R., Yamakawa H., Ohara O.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                       P35749; 000396; 094944; P78422; 01-JUN-1994 (Rel. 29, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Myosin heavy chain, smooth muscle isoform (SWMHC) MYH11 OR KIAA0866.
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                                                                                                                                         1746 KGADERCKKAMADAARLADELRAEQDHSN 1774
                                                                                                                   891 QGAGHPGELVLAPKQGQPLHIRVTPDHEN 919
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                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata;
Mammalla; Butheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-1266 FROM N.A.
                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissue=Brain;
                                                                                                                                                                                                MYHB HUMAN
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subfragment (S2).
-!- SMILARITY: Contains 1 myosin-like globular head domain.
-!- SIMILARITY: Contains 1 IQ domain.
-!- DATABASE: NAME-Atlas Genet. Oytogenet. Oncol. Haematol.;
-|- DATABASE: NAME-Atlas Genet. Cytogenet. Owcol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/WYH11ID43.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 KTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVL 126
artery, bladder, esophagus and trachea.
DOAAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
                                                                                                                DISEASE: A chromosomal rearrangement, known as pericentric inversion Inv(16) (p13,q22), Produces a fusion protein that consists of the 165 N-terminal residues of CBF-beta (PEPB2) with the tail region of MHALL. This rearrangement is associated with acute myeloid leukemia of MHEO subtype.

MISCELLARBOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 168; Mismatches 301; Indels 166; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0193; MYOSINHEAVY.
PRODOM; PRO0195; MYOSIN-Head; 1.
SWART; SM00015; IQ; 1.
PROSITE; PS50096; IQ; 1.
PROSITE; PS50096; IQ; 1.
MYOSIN; MASCLE protein; Coiled coil; Thick filament; Actin-binding; Protecoin; Chromosomal translocation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLED COLL (POTENTIAL).
CARBOXYL-TERMINAL.
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
EEK -> NSE (IN REF. 4).
T -> S (IN REF. 4).
T -> S (IN REF. 4).
T -> L (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB020673; BAA74889.2; ALT INIT.
EMBL; D10667; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 160745; -.
GO; GO:0005859; C:muscle myosin; TAS.
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
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Pfam; PF00063; myosin head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF001548; AAC31665.1; -.
EMBL; U91323; AAC35212.1; -.
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1786 1786
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1972 AA; 227338 M
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EMBL; X69292; CAA49154.1;
HSSP; P10587; 1BR2
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Matches 195;
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RY Wolecular Cloning and expression of mutine smooth muscle myosin heavy Chains. Bothye Res Commun. 232:313-316(1997).

RY TISSUE-Urenus Story 1-56 FROW N. RY MAINO W. Clson E.N., Manno J.M., Carpisal P. Lidgon K.L., Derisaamy M., Clson E.N., Manno J.M., Carpisal P. Lidgon K.L., Derisaamy M., Clson E.N., Manno J.M., Carpisal P. Lidgon K.L., Derisaamy M., Clson E.N., Manno J.M., Carpisal P. Lidgon K.L., Derisaamy M., Clson E.N., Manno J.M., Carpisal P. Lidgon K.L., Derisaamy M., Clson E.N., Manno J.M., Carpisal P. Lidgon K.L., Manno H. Pujii H., Aikwa M., Manno J.M., Carpisal P. Lidgon K.L., Manno H., Pujii H., Aikwa M., Manno J.M., Carpisal P. Lidgon K.L., Wasaki Y., Magai R., Peferential Aldferentials of Playmouse amphysional carcinome cells into smooth muscle cells. Use of retinoic acid and antisense against R. R. Carping M., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno H., Manno
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                                                                                                                                                                                                                                            RTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKET 160
                                                                                                                                                                                                                                                              867 ROOKAETELKELE------QKHTQLAEEKTL---LQEQLQAETELYAESEEMR 910
                                                                                                                                                                                                                                                                                            911 VR-----LAAKK-----OELEEILHEMEARLEEEEDRRQOLOAERKKWAQOMLDLEEQ 958
                                                                                                                                                                                                                                                                                                                                                         TQKLREEEEKLKAVT-----YKSKEDRQKLLKLEVDFEHKASRFSQEH 313
                                                                                                                                                                                                                                                                                                                                                                                                                                  356 EELQELREKIAKGECGNSSLMAEVESLRKRV---LEMEGKDEEI-TKTEAQCRELKKKLQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 V-----VKSRVKELE------CSESRLEKAELSLKDDLTKLKSFTVMLVDERKNM 514
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                          10.
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
RETHYLATION (TRI-) (POTENTIAL).
RGNEASFVPSRRAGGRRVIENTDGSEEEMDARDSDFNGTKA
                                                                                                                                                                                                                                                                                161 YRRMLEQLLLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERER-----LKKKL
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                                                                                                                                                                  tch 7.4%; Score 449; DB 1; Length 1972; al Similarity 23.5%; Pred. No. 8.6e-08; 203; Conservative 167; Mismatches 292; Indels 202; Gaps
Calmodulin-binding; ATP-binding; Methylation; Multigene family;
                                                                                                  SE -> GPPPGETSQ (in isoform 2).
/FTId=VSP 003346.
N -> D (IN REF. 3).
A -> V (IN REF. 2).
Q -> K (IN REF. 2).
WM; A1398E3F5B11F15A CRC64;
                   MYOSIN HEAD-LIKE
                                                                                                                                                 227026
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161
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.lmodulin-~....ternative splicing.
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1972
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CONFLICT
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                                                                                                                                                SEQUENCE
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                                                                        1532 KSKRALETOMEEMKTOLEESEDDVOATEDAKLRLEVNMOALKGOFERDLOARDEONEEKR 1591
       761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2).
-!- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
-!- SIMILARITY: Contains 1 myosin-like globular head domain.
714 AKSRDLQAEVQALKEKIHE----LMNKEDQLSQLQVDYSV------LQQRFMEEETKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of the CDNA encoding the myosin heavy chain of a vertebrate cellular myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 86:7726-7730(1989).
-!- FUNCTION: Cellular myosin appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, nonmuscle (Cellular myosin heavy chain) (NMMHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB-Intestinal epithelium;
MEDLINE-90046668; Pubmed-2813355;
Shoher R.V., Conti M.A., Kawamoto S., Preston Y.A., Brill D.A.,
Adelstein R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE, PS50096; 10, 1.
Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled coil; Multigene family.

DOMAIN 1 778 MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1959 AA
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                                                                                                                                                                                              1592 RQLQRQLHEYETELE-DERKQRAL 1614
                                                                                                                                                762 KNMGREVLNLTKELELSKRYSRAL
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InterPro; IPR0010648; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002228; Myosin_Cail.
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SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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15-MAR-2004
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us-10-788-793-2.rsp

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    471
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                                                                                                                                                                                                                         920 LEARVEEE---EERCQ-----HLQAEKKK--------MQQNIQELEEQLEEEES 957
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                                                                                                         40 KANRKEEDVMASGTIKRHLKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHM 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 SKELRLEVEKLOKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTK----DLLNELEV-
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                                                                                     Gaps
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                                                          Query Match 7.4%; Score 447.5; DB 1; Length 1959; Best Local Similarity 22.2%; Pred. No. 9.5e-08; Matches 224; Conservative 192; Mismatches 344; Indels 247;
837 1925 COLLED COLL (POTENTIAL).
174 181 ATTP (POTENTIAL).
654 676 ACTIN-BINDING.
1959 AA; 226502 MW; APSCR6086FD3A1A1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Short;
Isoid=PBOG22-2; Sequence=VSP 000765;
ISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
OF HODGKIN'S DISEASE.
SIMILARITY: Contains 2 CAP-Gly domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Peripheral blood monocytes;
MEDLINE=92289675; PubMed=1600942;
Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M., Cerletti N., Sorg C., Odink K., Tarceay L., Wiesendanger W., de Wolf-Peeters C., Shipman R.;
"Restin: a novel intermediate filament-associated protein highly expressed in the Reed-Sternberg cells of Hodgkin's disease.";
[2]
                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Keetin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-Sternberg intermediate filament associated protein).
                                  : | | : : | | : | | 131
1699 A-----QQERDELADEIANSSGKGALAMEEKRLEARI 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
-!- SUBCELLUAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE CYTOSKELETON.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 179838; C: endosome; TAS.

MIM; 179838; C: endosome; TAS.

GO; GO:0005768; C: endosome; TAS.

GO; GO:0015630; C: endosome; TAS.

GO; GO:0015630; C: endosome; TAS.

GO; GO:0015630; C: endosome; TAS.

GO; GO:0006817; Endocortubule binding; TAS.

GO; GO:0006899; P: nonselective vesicle transport; TAS.

InterPro; IPR001878; ZAP-GIY.

InterPro; IPR001878; ZAF CGHC.

PROSTIE; PR00045; CAP-GIY.

PROSTIE; PS00245; CAP-GIY.

PROSTIE; PS00245; CAP-GIY.

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PROSTIE; PS00245; CAP-GIY
SWIPWMRKRENGPSTPQEKGPRPNQGAGHPGELVLAPKQGQPLHIRV
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Pierre P., Scheel J., Rickard J.B., Kreis T.B.;
"CLIP-170 links endocytic vesicles to microtubules.";
Cell 70:887-900 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
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IsoId=P30622-1; Sequence=Displayed;
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EMBL; M97501; AAA35693.1; --
PIR; 822695; 822695.
MIM; 179838; --
                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                  647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 AVTYKSKEDROKLIKLEVDFEHKASRFSQEHEEMNAKLANQESHNRQLR---LKLVGLSQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             883
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                                                                                                                                                                                                                                                                                                                                                   1001 E-----KKMETSHNQCQELKARYERATSETKTKHEEIL-----QNLQKTLLDTEDKLKG
                                                                                                                                                                                                                                                                                                         536 SLLQ-EISSLQEKLEVTRTDHQR-EITSLKEHFGAREETHQKEIKALY----TATEKLSK
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Best Local Similarity 22.3%; Pred. No. 7.2e-08;
Matches 196; Conservative 187; Mismatches 329; Indels 166; Gaps
                                                                                                                                                                                                                       34 EDAKKNKANRKEEDVMASGT-----IKRHLKPSGESEKKTKKSVELSKE--DLIQLL
                                                                                                                                                                                                                                                                                                                                     EDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTVYELENEKHK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 LNKNFKVEQGKVMDVTE--KLIEESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  586 CELSCSVDLLKKRLDGIEEVEREINRGRSCKGSEFTCPEDNKIRELTLEIERLK----KR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642 LOQLEVVEGDLMKTEDEYDQLEQKFRTEQ---DKANFLSQQLEEIKHQMAKHKAIEKGBA
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Coiled coil; Repeat; Alternative splicing
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                                                                                                       /FTIG=VSP 000765.
D -> E (IN REF. 2).
W; 0A4F166DD94254E8 CRC64;
                                                                                             (in isoform Short)
           CAP-GLY 1.
SER-RICH.
CAP-GLY 2.
SER-RICH.
COLLED COIL (POTENTIAL).
CCHC-BOX.
Missing (in isoform Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     759 TKNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVD 796
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crotubule;
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Cytoskeleton;
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                                                                                                                                                                                                                                                 R Pfam; PF00612; IQ; I.
R Pfam; PF00135; Myosin_head; 1.
R Pfam; PF00136; Myosin_tai; 1.
R Pfam; PF01276; Myosin_tai; 1.
R Pfam; PF01576; Myosin_tai; 1.
R PRINTS; PR00193; MYOSINHEAVY.
R PRODOM; PD000355; myosin_head; 1.
R SMART; SM00015; IQ; 1.
R SMART; SM0016; IQ; 1.
R SMART; SM00142; MYS; 1.
R SMART; Muscle protein; Coiled coil; Thick filament; Actin-binding; Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; M T DOMAIN 785 807 IQ.
T DOMAIN 785 807 IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                          Lyctoragus cuntocutus (kabbil).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQ.
COILED COIL (POTENTIAL).
CARBOXYL-TERMINAL.
ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
SIMILARITY: Contains 1 IQ domain.
||:| : : ||||
----ELQLKENKRQLSSSSGNTDTQAD 1302
                                                                                                                           01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, smooth muscle isoform (SMMHC)
                                                                                  1972 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; SpectrIn.
                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last seq
                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit)
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                                                                                  STANDARD;
                                                                                                                                                                                                                              NCBI_TaxID=9986;
           1274 LKVKNL
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                                                                                 MYHB RABIT
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Db	PESTLY 12  RASO GYRAB  THE COTT-2010 (Rel. 40, Created)  DY 16-007-2010 (Rel. 40, Created)  DY 16-007-2010 (Rel. 40, Created)  DY 16-007-2010 (Rel. 40, Created)  DY 10-007-2011 (Rel. 40, Created)  DY 10-007-2011 (Rel. 40, Crea	e a
FT   MOD_RES   129   129   METHYLATION (TRI-) (POTENTIAL).     SQ   SEQUENCE   1972   AA;   227318   WW;   2061A22428B66AC CRC64;     Query   Match   7.3%;   Score   445;   DB   1;   Length   1972;     Best Local Similarity   21.5%;   Pred.   No. 1.2e-07;     Matches   248;   Conservative   164;   Mismatches   333;   Indels   406;   Gaps   44;     Qy	123 LRVLHRDAILAGGE - KSIGEDVYEKPISELDRIEBEKOKETYRRHEGOLL	1723 GRNALQDEKRRLBARIAQLEBELEBEGGNMEAMSDRVRKATQQAEQLSNBLATERSTAQK 696 GEAVSQEAELRHRFRLEEAKSRDLQAEVO ::: :

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SEQUENCE FROM N.A.
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                                                                                                                                                       VELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEV-----LEAHYGSAEPEKV 122
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                                                                                                                                                                                                                                                                                                                                                                  174 CHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLK-----KLLEQEKAYQARKE 225
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732 KDYKTLAKEQALNRISEIASEIFSEFTDGKYSNVIVRAEENKTKLFVVYEGKEV
  208;
Conservative 162; Mismatches 266; Indels
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Matches 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 94:559-571(1998).
-!- FUNCTION: Muscle contraction.
-!- SUBUNIT: Muscle contraction.
-!- SUBUNIT: Muscle contraction.
-!- SUBUNIT: Muscle contraction.
-!- SUBUNIT: Muscle contraction.
-!- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 and 2 regulatory light chain subunits (MLC-2).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
-!- MISCELLANBOUS: Each myosin heavy chain can be split into 1 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 1-818, AND REVISIONS 204-215.
MEDLINE-98412652; PubMed-9741621;
                                                                                                               "Complete primary structure of vertebrate smooth muscle myosin heavy chain deduced from its complementary DNA sequence. Implications on topography and function of myosin.";
J. Mol. Biol. 198:143-157(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meromyosin (LMM) and I heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (SI) and 1 rod-shaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ; 1. Wyosin; Muscle protein; Colled coll; Thick filament; Actin-binding; Myosin; Muscle protein; Calmodulin-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the
                                      Yanagisawa M., Hamada Y., Katsuragawa Y., Imamura M., Mikawa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dominguez R., Freyzon Y., Trybus K.M., Cohen C.; "Crystal structure of a vertebrate smooth muscle myosin motor and its complex with the essential light chain: visualization pre-power stroke state.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maita T., Onishi H., Yajima E., Matsuda G.;
Mahino adid sequence of the amino-terminal 24 kDa fragment
"Any clain of Chicken gizzard myosin.";
J. Biochem. 102:1133-145(1987).
                                                                                                                                                                                                                                                                                                                                                                             Masaki T.;
Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases
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MEDLINE=88118918; PubMed=2892941;
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InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
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SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
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Pfam; PF00063; myosin_head; 1.
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Pfam; PF01576; Myosin ta
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1BR2; 09-SEP-98.
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INIT_MET
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MYOSIN HEAD-LIKE.  10.  RODLIEE TAIL (SZ AND LAM DOMAINS). COLIED COIL (POTENTIAL).  ATP. ACTIN-BINDING. ACTIN-BINDING. BEJOCKED. METYLATION (TRI-) (POTENTIAL). MISSING (IN REF. 3). KUTSITQGPSFS -> RTPASLKVHLFP (IN REF. 1).	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98361239; PubMed=9697774; Simonsen A., Lippe R., Christoforidis S., Gaullier J.-M., Brech A., Callaghan J.M., Toh B.-H., Murphy C., Zerial M., Stenmark H.; "EEAl links PI(3)K function to Rab5 regulation of endosome fusion.";
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MEDLINE=95286647; PubMed=7768953;
Mu F.-T., Callaghan J.M., Steele-Mortimer O., Stenmark H.,
Parton R.G., Campbell P.L., McCluskey J., Yeo J.-P., Tock B.P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "EEA1, an early endosome-associated protein. EEA1 is a conserved alphe-halical peripheral membrane protein flanked by cysteine fingers' and contains a calmodulin-binding IQ motif.";
J. Biol. Chem. 270:13503-13511(1995).
                                                                                                                                                                                                                                             834 MSNLRQVGLKKPMERSSV---LDRYPPAA-----NELTMRKSWIPWMRKREN
                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Early endosome antigen 1 (Endosome-associated protein p162)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.-H., Stenmark
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INTERACTION WITH STX6, AND SUBCELLULAR LOCATION.
MEDLINE=99436077; PubMed=10506127;
Simongen A., Gaullier J.-M., D'Arrigo A., Stenmark H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                        PRT; 1411 AA
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MEDLINE=99421752; PubMed=10491193;
Callaghan J.M., Nixon S., Bucci C., Toh B.
"Direct interaction of ERAL with Rabsb.";
Eur. J. Biochem. 265:361-366(1999).
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                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                sapiens (Human)
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AC Q15075; Q14221;
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-!- SUBCELDULAR LOCATION: Cytoplasmic and peripheral membrane protein associated with early endosmes.
-!- DOMAIN: The FYVE-type in consones and the phosphatidylinositol 3-phosphate.
-!- DISEASE: Antibodies against EEA1 are found in sera from patients
                                                                                                                          MUTAGENESIS OF ASF-1352; ASN-1357; 1367-VAL-THR-1368; ARG-1375 AND ARG-1400, HOMODIMERIZATION, AND INTERACTION WITH PHOSPHATIDYLINOSITOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with subacute cutaneous lupus erythematosus and other autoimmune
                                                                                                                                                                                                                                                                                 Kutateladze T.G., Ogburn K.D., Watson W.T., de Beer T., Emr S.D.,
Burd C.G., Overduin M.;
"Phosphatidylinositol 3-phosphate recognition by the FYVE domain.";
Mol. Cell 3:805-811(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kauppi M., Simonsen A., Bremnes B., Vieira A., Callaghan J.M., Stenmark H., Olkkonen V.M.; "The small GTPase Rab22 interacts with BEA1 and controls endosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                        (7)
WINDAGENESIS OF TRP-1349; CYS-1358; PHE-1365; ARG-1370; ARG-1371;
HIS-1372; HIS-1373; CYS-1374; ARG-1375; CYS-1377; GIY-1379; CYS-13
ARG-1400 AND CYS-1405, SUBCELLULAR LOCATION, AND INTERACTION WITH
PHOSPHATIDYLINOSITOL 3-PHOSPHATE.
MEDLINE=20387352; Pubmed=10807926;
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RABSC.
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MEDLINE=21143489; PubMed=11230696;
Kutateladze T.G., Overduin M.;
"Structural mechanism of endosome docking by the FYVE domain.";
Science 291:1793-1796(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaullier J. M., Roenning E., Gillooly D.J., Stenmark H.; Interaction of the EAH FYVE finger with phosphatidylinositol 3. Phosphate and early endosomes. Role of conserved residues."; Biol. Chem. 275:14595-24600(2000).
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S
ne Rab5 effector EEA1 interacts directly with syntaxin-6."; Biol. Chem. 274:28857-28860(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawe D., Corvera S., Lambright D.G., Rultivalent endosome targeting by homodimeric EEAL."; Mol. Cell 8:947-958(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merithew B., Stone C., Eathiraj S., Lambright D.G., "Determinants of Rab5 interaction with the N terminus endosome anticen 1.";
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HOMODIMERIZATION, AND INTERACTION WITH
MEDLINE-22499593; PubMed-12493736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11870209;
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J. Biol. Chem. 278:8494-8500(2003),
                                                                                                                                                                                                                                        MEDLINE=99322673; PubMed=10394369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane trafficking.";
J. Cell Sci. 115:899-911(2002)
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FT MUTAGEN 1400 1400 R->G: STRONGLY REDUCES FT AND ABOLISHES ENDOSOMAL LOCATION. FT AND ABOLISHES ENDOSOMAL LOCATION. FT CONFLICT 255 255 C-> S (IN REF. 1). FT CONFLICT 258 259 LQ-> S (IN REF. 1). FT CONFLICT 277 A-> S (IN REF. 1). FT CONFLICT 278 24 A-> S (IN REF. 1). FT CONFLICT 276 277 A-> S (IN REF. 1). FT CONFLICT 277 A-> S (IN REF. 1). FT CONFLICT 277 A-> S (IN REF. 1). FT CONFLICT 277 A-> S (IN REF. 1). FT CONFLICT 275 270 D-> E (IN REF. 1). FT CONFLICT 275 270 D-> E (IN REF. 1). FT CONFLICT 570 520 D-> E (IN REF. 1).	Query Match 7.2%; Score 440; DB 1; Length 1411; Best Local Similarity 19.5%; Pred. No. 1.2e-07; Matches 258; Conservative 258; Mismatches 474; Indels 334; Gaps 51;	Qy 35 DAKKNKANRKEEDVMASGTIKRHLKPSGESEKKTKKSVELSKEDLIQLLSIMEGELQ 91	Qy 92 AREDVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQE-135	136	Db 291 QKLKSSVNELTQKNQTLTENLLKKE-QDYTKLEEKHNEESVSKKNIQATLHQKDLDCQQL 349		350 QSR		277	465	Qy 330 LRLKLVGLSQRIEELEETNKSLQKAEEELQELREKIAKGECGNSSLMAEVES 381		Qy 382 LRKRVLEMEGKDEEITKTEAQCRE-LKKKLQEEEHHSKELRLEVEKLQKRMSELEKLEEA 440	573	QY 441 PSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSRVKELECSESRLEKAELSLKD 495	Db 630 LNESKEKVSQLDIQIKAKTELLLSAEAAKTAQRADLQNHLDTAQNALQDKQQELNK 685	QY 496 DLTKLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNPKVEQGKVMDV 542	989 1		Qy 600 DGIEEVERBINRGRSCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDL 652	DD 803 TKQEBEKQILKQDFETLSQETKIQHEELNNRIQTTVTELQKVKMEKEALMTELSTVKDKL 862	Qy 653 MKTEDEYDQLEQKPRTEQDKANFLSQQLEEIKHQMAKHKALEKGEAVSQEAELRHR 708		709 FRLEBAKSRDLQAEVQALKEKIHELMNKEDQLSQLQVDYSVLQQRFMEEETKNK	Db 919 LEKEKEASHQLKLELNSMQEQLIQAQNTLKQNEKEEQQLQGNINELKQSSEQKKK 9/3 Qy 763 NMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPVASTGVQTEAVCGDAAEEETPAVF 822	
CC or send an email to license@isb-sib.ch).  CC	X GO; GO:0005769; C:early endosome; TAS. X GO; GO:0005624; C:membrane fraction; TAS. X GO; GO:0005545; F:phosphatidylinositol binding; TAS. X GO; GO:0005699; P:nonselective vesicle transport; TAS.		S SWART; SM0064; FYUE; 1.  R SMART; SM0355; ZNF_CZH2; 1.  R PROSITE; PSSO178; ZF FYUE; 1.	REGISTE: FSOUCE; INTO FINGER C2H2_1 1. REGISTE: PSSSUES; ZINC FINGER C2H2_2 1. Antigen; Metal-binding; Zinc; Coiled coil; Zinc-finger; 3D-structure.	r DOMAIN 74 1348 COILED COIL (POTENTIAL).	DOMAIN 93/ 1032 GLN/GLD/LES-KICH.   DOMAIN 1093 1231 GLU/LYS-KICH.   XN FING 41 64 C242_TYPE.	ZN_FING 1352 1410 MUTAGEN 39 39	T MUTAGEN 41 41 P->A: STRONGLY REDUCES INTERACTION WITH	MUTAGEN 42 42	MUTAGEN 44 44	MUTAGEN 47 47	MUTAGEN 60 60 Y->A: STRONGLY REDUCES INTERAC RABSC.	MUTAGEN 1349 1349	MUTAGEN 1352 1352	MUTAGEN 1357 1357 N->D: REDUCES PHOSPHATIDYLINOSITOL 3- PHOSPHATE BINDING AND ENDOSOMAL LOCAT	MUTAGEN 1358	MUTAGEN 1365 1365	MUTAGEN 1367 1368	AND ENDOSOMAL LOCATION.  R->A: ABOLISHES ENDOSOMAL LOCATION. FT MUTAGEN 1371 R->A: ABOLISHES PHOSPHATIOYLINOSITOL 3-	MUTAGEN 1372 1	MUTAGEN 1373 1373	MOIAGEN 13/4 13/4	MUTAGEN 1375 1375	T MOTAGEN 13/1 C-74: ADDITIONS AND ENDOSOMAL LOCATION. T MOTAGEN 1378 G->4: ABOLISHES PHOSPHATIDYLINOSITOL 3-	1385 1385	

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entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 SEDAKKNKANRKEE-----DVMASGTIKRHLKPSGESEKKTKKSVELSKEDL-IQLLSIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 YEKPISELDRLE-----EKQK-----ETYRRMLEQLLLAEKCHRRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                         Problem, France...
SMART; SM00015; IQ; 1.
SMART; SM00042; MYSC; 1.
PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled coil; Thick filament; Actin-bindi Calmodulin-binding; ATP-binding; Methylation; Multigene family.
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COILED COIL (POTENTIAL)
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Conservative 181; Mismatches 338;
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ACTIN-BINDING.
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InterPro; IPR002017; Spectrin.
Pfam; PF00612; IQ; 2.
Pfam; PF00513; Myosin_head; 1.
Pfam; PF012736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINTEAVY.
ProDom; PD000355; Myosin_head; 1.
                                                                                                                                                                               HSSP; P13538; 2MYS.
InterPro; IPR000048; IQ region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
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Matches 223;
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1. Mol. Biol. 190.291-117(1986).

2. Mol. Biol. 190.291-117(1986).

3. Mol. Biol. 190.291-117(1986).

4. FUNCTION: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC).

5. And 2 regulatory light chain subunits (MLC).

5. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

6. I- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.

6. CHANGELLANGOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                                                                  ---GNQ------NKLIQELKTAKATLEQDSAKKEQQLQERCKALQDIQKEKSLKEK 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVGM-----KKH---EENEAKLTMQIT----ALNENLGTVKKEWQ--SSQRRVSELEK 1269
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| ||: |:
-----QIEALQGEL-----KIA 985
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                                                  IRKSFQEENHIMSNLRQVGLKKPMERSSVLDRYPPAANELTMRKSWIPWMRKRENGPSTP
                                                                                      ----AAQELAAEKEKİSVL---QNNYEKS
                                                                                                                        QEKGPR-PNQGAGHPGELVLAPKQGQPLHIRVTPDHENSTATLEITSPTSEEFFSSTTVI
                                                                                                                                                            ------DLKSVEEKLSLAQEDLISNRNQI
                                                                                                                                                                                                PTLGNOKPRITIIPSPNVMSQKPKSADPTLGPERAMSP-----VTITTISREKSPEGG
                                                                                                                                                                                                                                                                                                                                             ---TVPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTAEK
                                                                                                                                                                                                                                                                                                                                                                                                                   EVSTGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTRGTQSVSGQDGSSQRPTPTRIP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy chain gene. Evidence against intron-dependent evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87060988; PubMed=3783701;
Strehler E.E., Strehler-Page M.-A., Perriard J.C., Periasamy M.,
Nadal-Ginard B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                               1178 KADSLKAAVEQEKRNOQILKDOVKKEEEELKKEFIEKEAKLHSEIK----
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01-OCT-1989 (Rel. 12, Last sequence update)
15-WAR-2004 (Rel. 13, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic.
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                                                                         Nadal-Ginard B.; "Complete nucleotide and
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qq	1304	:::      :  :   1304 RSKQAFTQQIEELKRQLEBENKAKNALAHALQSSRHDCDLLREQYEBEQEGKAELQRALS 1363
ò	435	SKSECTQLHLNLEKEK 459
qq	1364	1364 KANSEVAQWRTKYETDALQRTEELEEAKKKLAQRLQDSEEQVEAVNAKCASLEKTKQRLQ 1423
ò	460	NLTKDLINELEVVKSRVKELECSESRLEKAELSLKDDLT 498
qq	1424	1424 GEVEDLMVDVERANSLAAALDKKQRNFDKVLAEWKTKCEESQAELEAALKESRSLSTELF 1483
δλ	499	KLKSFTVMLVDERKNMMEKIKQBERKVDGLNKNFKVEQGKVMDVTEKLIEESKKLLK 555
ą	1484	KLKNAYEEALDQLETVKRENKNLEQEIADLTEQIAENGKSIHELEK 1529
ò	556	LKSEMEEKEYSLIKERDELMGKLRSEEERSCELSCSVDLLKKRLDGIEEVEREINRGRSC 615
qa	1530	1530 SRKQMELEKADIQMALEEAEAALEHEEAKILRIQLE-LTQVKSEI 1573
δ	616	616 KGSEFTCPEDNKIRELTLEIERLKKRLQQ-LEVVEGDLMKTEDEYDQLEQKFRTEQD 671
QQ	1574	DRKIAEKDEEIEQLKRNYQRTVETMQGALDAEVRSRNEAIRLKKKNGGDLN 1624
λ	672	672 KANFLSQOLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEEAKSRDL 719
q	1625	: EIBIQLSHANRQAAETIKHLRSVQGQLKDTQLHLDDALRGQEDLKEQLAIVERRANLL 1682
λõ	720	QAEVQALKEKIHELMNKEDQLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTKEL 775
q	1683	
λo	176	ELSKRYSRALRPSGNGRRMVDVPVASTGVQTBAVCGDAAEBETPAVFIRKSFQE 829
qq	1743	:     :
6y	830	ENHIMSNLRQVGLK 843
qa	1794	LOHRLDEAEQLALK 1807
Search Job tir	ch complet time : 42	Search completed: September 7, 2004, 13:13:58 Job time : 42 secs

Q9csl6 mus musculu Q8bqwl mus musculu Q9fj35 arabidopsis

Q9esvl rattus norv

007569 entamoceda h 099968 homo sapien 08157 plasmodium 02015 gallus gall 02015 gallus gall 091144 plasmodium 07380 saccharomyc 091121 aequipecten 091120 aequipecten 09120 aequipecten 09120 aequipecten 09120 aequipecten 09131 aequipecten 09131 aequipecten 09131 aequipecten 08580 mus musculu 08580 mus musculu 08580 mus musculu 08581 plasmodium 06371 rattus norv 063731 rattus norv

Q26079 placopecten O93522 xenopus lae Q8ir55 drosophila Q26080 placopecten

Q8r384 mus musculu Q9vy43 drosophila Q04834 xenopus lae

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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1 MRSRNQGGESSSNGHVSCPKSSIISSDGGKGPSEDAKKNKANRKEEDVMASGTIKRHLKP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Wistar;
MEDLINE-22100428; PubMed=12055638;
MEDLINE-22100428; PubMed=12055638;
Nagano T., Yoneda T., Hatanaka Y., Kubota C., Murakami F., Sato M.;
Filamin A-interacting protein (FILIP) regulates cortical cell
migration out of the ventricular zone.";
NAC. Cell Biol. 4:495-501(2002).
EMBL; AB055759; BAC00851.1; -.
InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 1212 AA; 137752 MW; AIDSB9C5AF7D4F80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 6082; DB 11; Length 1212; ilarity 100.0%; Pred. No. 9.2e-232; Conservative 0; Mismatches 0; Indels 0;
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Q9ESV1
Q9CSL6
Q8BQW1
Q9FJ35
Q07569
Q99968
Q8T5C7
Q8IHP3
Q02015
                                                                                                            Q07380
Q9NJ22
Q9NJ21
Q9NJ20
Q17042
P92021
Q19658
Q8VDD5
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Q22869
Q9NJ23
Q8R384
Q9VY43
Q26079
Q91R55
Q26080
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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                      Local Similarity
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Q96sk6 homo sapien
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Q86tc3 homo sapien
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                                                                         September 7, 2004, 13:07:18; Search time 152 Seconds (without alignments) 2515.843 Million cell updates/sec
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                                                                                                                                             1 MRSRNQGGESSSNGHVSCPK......KIELKKSAASSTASLGGGKG 1212
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Q81um3 homo s
Q13597 homo s
Q86v48 homo s
Q9feth1 homo s
Q99ng3 mus m
Q8r4u7 mus m
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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QBK7TB0
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Score

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Result

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61 TSGECERKTKKSLELSKEDLIQLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEP 120 301 VDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLTQRIEELEETNKNLQKAEEELQ 360 421 IRLEVEKLQKRMSELEKLEEAFSKSKSECTQLHINLEKEKNLTKDLINELEVVKSRVKEL 480 540 900 60 PSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEP 119 120 EKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTV 179 239 240 299 241 VKLKSFALMLVDERQWHIEQLGLQSQKVQDLTQKLREEEEKLKAITSKSKEDRQKLLKLE 300 300 VDFEHKASRFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAEEELQ 359 360 ELREKIAKGECGNSSLMAEVESLRKRVLEMEGKDEBITKTEAQCRELKKKLQEEEHHSKE 419 600 DGIEEVEREINRGRSCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDLMKTEDEY 659 420 LRLEVEKLQKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSRVKEL 479 480 ECSESRIEKAELSLKDDLTKLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNFKVEQGKV 539 1 MRSRNQGGESSSNGHVSCPKSSIISSDGGKGPSEDA-KKNKANRKEEDVMASGTIKRHLK 59 121 EKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTV 240 VKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKLLKLE 541 MDVTEKLIEESKKLIKLKSEMEEKVYNLTRERDELIGKLKSEEEKSSELSCSVDLLKKRL 180 YELENEKHKHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQARKEKENAKRLNKLRDEL 481 ECSESRLEKAELSLKDDLIKLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNFKVEQGKV 540 MDVTEKLIEESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKRL 1; Gaps Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1201 ASSTASLGGGKG 1212

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120 179 239 240 299 300 359 360 419 420 479

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DOLEOKFRTEQDKANFLSQQLEEIKHQIAKNKAIEKGEVVSQEAELRHRFRLEEAKSRDL
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 EKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKOKETYRRMLEQLLLAEKCHRRTV
                                                                                                                                                   YELENEKHKHTDYMNKSDDFTNLLEQERERLKKLLEQEKAYQARKEKENBKRLNKLRDEL
                                                                                                                                                                                                  VKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKLLKLE
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                                                        EKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTV
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                                                                                                                                               VGLKKPMERSSVLDRYPPAANELTMRKSWIPWMRKRENGPSTPQEKGPRPNQGAGHPGEL
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Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Fobo
Wambutt A., Wienann S.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; ABJ32009; CABB9912.1; -.
InterPro; IPRO00533; Tropomyosin.
PRINTS; PRO0194; TROPOMYOSIN.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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SEQUENCE 1177 AA; 134826 MW; D791D2A35FD10E4B CRC64;
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Last sequence update)
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01-UUN-2003 (TrEMBLrel. 24, Created
01-UUN-2003 (TrEMBLrel. 24, Last se
01-OCT-2003 (TrEMBLrel. 25, Last an
Hypothetical protein DKFZp451B134.
DKFZP451B134.
Homo sapiens (Human).
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Matches 1086; Conserv
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                           547 ELTCPEDNKIKELTLEIERLKKRLQQLEVVEGDLMKTEDEYDQLEQKFRTEQDKANFLSQ 606
                                                                                                          QLEEIKHQIAKNKAIEKGEVVSQEAELRHRFRLEEAKSRDLKAEVQALKEKIHELMNKED 666
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                                                                                  QLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEEAKSRDLQAEVQALKEKIHELMNKED 738
                                                                                                                                                               739 QLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVP 798
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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EMBL; D87257; BAC00833; Tropomyosin. PRINTS; FR001944; TROPOMYOSIN. S0352DP4F8236B40 CRC64;
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79.5%; Score 4838; DB 11; Length 96
Best Local Similarity 100.0%; Pred. No. 6.8e-183;
Matches 965; Conservative 0; Mismatches 0; Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Filamin-interacting protein S-FILIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                             799
                                                                                  619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 FTNLLEQERERLKKLLEQEKAYQARKEKENAKRLNKLRDELVKLKSFALMLVDERQMHIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 LIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEPEKVLRVLHRDAILAQEKSI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 GEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTVYELENEKHKHTDYMNKSDD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FINILEQERERLKKLLEQEKAYQARKEKENAKRINKLRDELVKLKSFALMLVDERQMHIE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 QLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKLLKLEVDFEHKASRFSQEHEEMNA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 QLGLQSQKVQDLTQKLREEEEKLKAITSKSKEDRQKLLKLEVDFEHKASRFSQEHEEMNA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 KLANQESHNRQLRLKLVGLSQRIEELEETNKSLQKAEEELQELREKIAKGECGNSSLMAE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 VESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRLEVEKLQKRMSELEKLE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSRVKELECSESRLEKAELSLKDDLT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 BAFSKSKSECTQLHLINLEKEKNLTKDLINELEVVKSRVKELECSESRLEKAELSLKDDLT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 KLKSFTVMLVDERKUNMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLIEESKKLLKLKS 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMEEKVYNLTRERDELIGKLKSEEEKSSELSCSVDLLKKRLDGIEEVEREITRGRSRKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLKSFTVMLVDERKNMMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLIEESKKLLKLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBEKEYSLTKERDELMGKLRSEEERSCELSCSVDLLKKRLDGIEEVEREINRGRSCKGS
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=20036619;
PubMed=10574462;
Nagase T., Ishkawa M., Nomura N., Ohara O.;
Nagase T., Ishkawa M., Kikuno R., Hirosawa M., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XV."
"Prediction of the coding sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999).
EBBL; ABO33101, BA86589.1; -.
Genew, HGNC:21015; FILIP1.
InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
"XX. mmn."
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 1140 AA; 130283 MW; 79EC2AE496556415 CRC64;
                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein KIAA1275 (Fragment)
Home sapiens (Human)
                                                                                                     PRT; 1140 AA
GTQSVSGQDGSSQRPTPTRIPMSK 1164
                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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1141
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	367 OS Homo sapient OC Eukaryota; 1	OX RN		487 RA Tanai H., K. RA Saito K., Yi RA Manho Y. 140	RT RL		607 KW Hypothetica. SQ SEQUENCE :	360 Onerv Match	667 Best Local Simi Matches 904;	ζ		OY 308 RFS 787 An 61 BE	70 0	847 UN 358 GEV	428	ZY ZZ ZZ ZZ ZZ ZZ ZZ ZZ ZZ ZZ ZZ ZZ ZZ Z	660 QY 488 KAI	967 Db 241 KAI	Oy 548 BES	Db 301 EE	609	361	1147   QY 668 TEC	17#	1207 QY 7.28 EA. 	788	541	848	  Db 601 RSE	Qy 908 PLF	Db 661 PLF
1 MLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKAVTYKSKEDRQKLLKLEVDFEHKAS	308 RFSQEHEEMNAKLANQESHNRQLRLKLVGLSQRIBELEETNKSLQKAEBELQELREKIAK : 			428 QKRMSELEKLEEAFSRSKSECTQLHLNLEKEKNLTKDLLNELEVVKSRVKELECSESRLE	KAELSLKDDLTKLKSFTVMLVDERKNNMEKIKQEERKVDGLNKNFKVEQGKVMDVTEKLI		EESKKLLKLKSEMEEKEYSLTKERDELMGKLRSEEERSCELSCSUDLLKKRLDGIEEVER	٠~	608 EINRGRSCKGSEFTCPEDNKIRELTLEIERLKKRLOOLEVVEGDLMKTEDBYDQLEOKFR (			728 EKIHELMNKEDQLSQLQVDYSVLQQRFMBEETKNKNMGREVLNLTKELELSKRYSRALRP		788 SGNGRRWVDVFVASTGVQTEAVCGDAAEETPAVFIRKSFQEENHIMSNLRQVGLKKPME		RSSVLDRYPPAANELTMRKSWI PWMRKRENGPSTPQEKGPRPNQGAGHPGELVLAPKQGQ	KSSVLDRYPPAANELTMRKSWIPWMRKRENGPSTPQEKGPRPNQGAGHPGELVLAPKQGQ	908 PLATRYTPDHENSTATLEITSPYSEEFFSSTTVIPTLGNOKPRITIIPSPNYMSOKREKSA 	DPTLGPERAMSPVT1TTISREKSPEGGRSAFADRPASPIOIMTVSTSAAPTEIAVSPESO		ο.		088 VITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTRGTQSVSGQ		1148 DGSSQRPTPTRIPMSKGMKAGKPVVAASGAGNLTKRQPRAETQSMKIELKKSAASSTASL 1		208 GGGKG 1212 	961 GGGKG 965		O96SK6 PRELIMINARY; PRT; 965 AA. O96SK6:	C-2001 (TrEMBLrel, 19. Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKKLLKLKSEMBEKEYSLTKERDELMGKLRSEBERSCELSCSVDLLKKRLDGIEEVER 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRGRSRKGSELTCPEDNKIKELTLEIERLKKKLLQQLEVVEGDLMKTEDEYDQLEQKFR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ODKANFLSQQLEEIKHQMAKHKAIEKGEAVSQEAELRHRFRLEEAKSRDLQAEVQALK 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSSVLDRYPPAANELTMRKSWIPWMRKRENGPSTPOEKGPRPNGGAGHPGELVLAPKOGO
                                                                                                                                                                                                                                                                                                                                                                                                                               VDEROMHIEQLGLOSOKVODLTOKLREEEKLKAVTYKSKEDROKLLKLEVDFEHKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCGNSSLMAEVESLRKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRLEVEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRGRSCKGSEFTCPEDNKIRELTLEIERLKKRLQQLEVVEGDLMKTEDEYDQLEQKFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (THELMINKEDQLSQLQVDYSVLQQRFMEEETKNKNMGREVLNLTKELELSKRYSRALRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AELSLKDDLTKLKSFTVMLVDERKNMMEKIKQERKVDGLNKOPKVEQGKVMDVTEKLI
                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                             Ora T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
3 (TrEMBLrel. 23, Last annotation update)
al protein FLJ14799.
ns (Human).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                     n CDNA sequencing project.";
(MAY-2001) to the EMBL/GenBank/DDBJ databases.
7705; BAB55310.1; -.
IPR000533; Tropomyosin.
al protein.
965 AA; 109200 MW; 25EB750B47E42433 CRC64;
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Conservative
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RE STEURNER FROM N. A.

RA ARAWAT T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAMANAT T., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arawawa T., Hara A., Tolopori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ratchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ratchi M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,

Rada K., Okido T., Furuno M., Anon H., Baldarelli M., Banch G.,

Rada I., Bolfelli D., Bolunga N., Carninci P., de Bonaldo M.F.,

Radain K., Okido T., Furuno M., Anon H., Baldarelli M., Manbar G.,

Radincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

R. Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,

R. Jyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,

R. Sazuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R. Sazuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

R. Hayashizaki Y., Topomyosin.

R. Mature 409:685-69012001.

R. Mature 409:685-69012001.

R. Mature 409:685-69012001.

R. Mature 409:685-69012001.

R. Mature 409:685-69012001.

R. Mature 409:685-69012001.

R. MINIS, PRO0194; TROPOMYOSIN.

R. NON TER G. M. Topomyosin.

R. NON TER G. M. Topomyosin.

R. SEQUENCE 610 AA, 70346 MM, 9B9EFC87F64FCE80 CRC64,
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                                                                                    STATLEITSPTSEFFSSTTVIPTLGNQKPRITIIPSPNVMSQKPKSADPTLGPERAMSP
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                                                                                                                                                                                                                                    421 VIITTFSREKTPESGRGAFADRPTSPIQIMTVSTSAAPAEIAVSPESQEMPMGRTILKVT
                                                                                                                                                                                                                                                                                                               PEKQTVPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSPGPAAEGVSPVITVRPVNVTAE
                                                                                                                                                                                                                                                                                                                                               481 PEKQTVPTPVRKYNSNANIITTEDNKIHIHLGSQFKRSPGTSGEGVSPVITVRPVNVTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 KEVSTGTVLRSPRNHLSSRPGASKVTST1T1TPVTTSSARGTQSVSGQDGSSQRPTPTR1
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                                                                                                                                                                                                                                                                                                                                                                                                                          KEVSTGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTRGTQSVSGQDGSSQRPTPTRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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41.5%; Score 2522.5; DB 11; Lengt.)
Best Local Similarity 98.1%; Pred. No. 6e-92;
Matches 506; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
5730485121Rik protein (Fragment).
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DPTLGPERAMSPVTITTISREKSPEGGRSAFADRPASPIQIMTVSTSAAPTEIAVSPESQ 1027
                                                                                                                                                                                                                                                                                                                                                                      901 DGSSQRPTPTRIPMSKGMKAGKPVVAAPGAGNLTKFEPRAETQSMKIELKKSAASSTTSL 960
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                             EVPMGRTILKVTPEKQTVPAPVRKYNSNANIITTEDNKIHIHLGSQFKRSPGPAAEGVSP
                                                                                                                                               VITVRPVNVTAEKEVSTGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTRGTQSVSGQ
                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A. SUGIYAMA T., Otsuki T., Suzuki Y., SEGUENCE FROM N.A. Sugahi K., Sugiyama T., Otsuki T., Suzuki Y., Nisogai T., Ota T., Hayashi K., Sugaho S., Shiratori A., Sudoh H., Sugawara M., Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Maranabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamati Y., Nagahari K., Masuho Y., Namono J., Wakamati T., Namono J., Wakamanagi T., Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

Hypothetical procesin.

SEQUENCE 653 AA; 72451 MW; 33379801AD14AC86 CRC64;
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61 TSGECERKTKKSLELSKEDLIQLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEP 120
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     EKVLRVLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQLLLAEKCHRRTV
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                                                                                      PSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to downregulated in ovarian cancer 1.
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335 VKLKSFALMLVDERQMHIEQLGLQSQKVQDLTQKLREEEEKLKALTYKSKEDRQKLLKLE
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Tashiro H. Yamazaki M., Watenabe K., Kumagai A., Itakura S.,

Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,

Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,

Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,

Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                PSGESEKKTKKSVELSKEDLIQLLSIMEGELQAREDVIHMLRTEKTKPEVLEAHYGSAEP
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
14-Prochetical protein FLJ39702 (Fragment).
16-Markaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
17-Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK097021; BAC094298.1; -.
Interpro; IRR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
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SEQUENCE 764 AA; 89785 MW;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUB=Skeletal muscle;
Revert-Ros F., Raya A., Granero F., Saus J.;
"Cloning and expression of GIP90, a protein down-regulated
"Cloning and expression of GIP90, a protein down-regulated
cells which interacts with GPBP.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, ANNI6206 J.;
TITOPOMYOSIN. TTOPOMYOSIN.
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01-MR-2003 (TrEMBLrel. 23, Last sequence update)
01-MR-2003 (TrEMBLrel. 24, Last annotation update)
GPBP-interacting protein 90.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                        22;
30.1%; Score 1828; DB 4; Length 76.
ilarity 50.7%; Pred. No. 1.7e-64;
Conservative 144; Mismatches 210; Indels
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                             Knapp R.C.,
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                                                                                            Wong K.K., Mok S.C.; "Cloning and sequencing of full length Doc1 and Doc2 mRNAs."; "Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; US3445; AAA98972.1; -.
                                                                                                                                                                DB 4; Length
                                                                                                                                                                       Best Local Similarity 46.3%; rrcu. nv. .... Matches 363; Conservative 140; Mismatches 216; Indels
                                                                                                                                  GO:0016459; C:myosin; NAS.
IENCE 752 AA; 87141 MW; D763B4E2806A3B0B CRC64;
                                            "Molecular cloning of differentially expressed genes epithelial ovarian cancer."; Gynecol. Oncol. 52:247-252(1994).
         SEQUENCE FROM N.A.
MEDINE=94148289; PubMed=8314147;
MCD L.NE S.C., Wong K.K., Chan R.K., Lau C.C., Tsao S.W.,
Berkowitz R.S.;
                                                                                                                                                               27.1%; Score 1645.5; DB 446.3%; Pred. No. 2.5e-57;
                                                                                    SEQUENCE FROM N.A.
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A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B. Buerow K.H., Schmefer C.F., Bhar N.K.,

A Alschul S.F., Zeeberg B. Buerow K.H., Schmefer C.F., Bhar N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hohat F.K.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

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Mhiting M., Madan A., Young A.C., Schwutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Dones S.J., Marra M.A.,

Brands M. M. Schillaka U., Smailus D.E., Schmerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051733; AAH5133.1; -.
GO; GO:0005743; AAH5133.1; -.
GO; GO:0005748; F:binding; IEA.
GO; GO:0006810; F:transport; IEA.
InterPro; IPR001993; Mitoch carrier.
PROSITE; PS00215; MITOCH CARRIER; 1.
SEQUENCE 1026 AA; 114616 MW; A8A11163CB24DF5A CRC64;
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Last annotation update)
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Matches 283; Conservative 143; Mismatches 302;
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MEDLINE=22388257; PubMed=12477932;
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01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                          EIKHOMAKHKAIEKGEAVSOEAELRHRFRLEEAKSRDLQAEVQALKEKIHEL--MNKEDQ 739
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KEYSLIKERDELMGKLRSEEERSCELSCSVDLLKKRLDGIEEVEREI-NRGRSCKGSEFT 621
                                   NDLRI---EDGISSTLPSKESRR------KGGLDYLKQVENETRNKSENEKNRN-- 282
                                                                                      CPEDNKIRELTLEIERLKKRLOQLEVVEGDLMKTEDEYDQLEQKFRTEQDKANFLSQQLE
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Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-Spleen;
Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAEKEV-----STGTVLRSPRNHLSSRPGASKVTSTITITPVTTSSTR 1139
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-----VPAPVRKYNSNANIITTEDNKIHIHLGSQPK-RSPGPAAEGVSPVITVRPVNV 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSQLQVDYSVLQQRFMEBETKNKNMGREVLNLTKELELSKRYSRALRPSGNGRRMVDVPV 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 L------RNREFALNNEN-----YSLSNR--QVSSPSFTNRRA--AKA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                800 ASTGVOTEAVCGDAAEEETPAVFIRKSFQEENHIMSNLRQVGLKKPMERSSVLDRYPPAA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 QEHS--KAW-----KGTSKPGTESGLKGKVEKTTRTFSDTTHGSVPSDPLGRADKASDTS 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           897 GELVLAPKQGQPL--HIRVTPDHENSTATLEITSPTSEEFFSSTTVIPTLGNQKPRITII 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYSLIKERDELMGKIRSEEERSCELSCSVDLLKKRLDGIEEVEREI-NRGRSCKGSEFT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 BIKLÓIKKOKELENGEVEGEDÁFLSSKGRHERTKFRGHGSEASVSKHTARELSPOHKRER 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 SETVFG-KRGHVLGNGSQVT-QAANSGCSKAIGALASSRRSSS----EGLSKGKKAANGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    582 BADNSCPNSKAPVLSKYPYSCRSQENILQGFSTSHKEGVNQPAAV--VMEDSSPHEALRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             640 RVIKSSGREKPDSDDDLDIASLVTAKLVNTTITPEPEPKPQPNSREKAKTRGAPRTSLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 955 PSPN-----VMSQKPKSAD------PTLGPERAMSPVTITTISREKSPEGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---RSAFADRPASPIQI----MTVSTSAAPTEIAVSPESQEVPMGRTILKVTPEKQT----
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                                                                                                                                                                                   323 QESHNRQLRLKLVGLSQRIEELEETNKSLQKAEEELQELREKIAKGECGNSSLMAEVESL
                                                                                                                                                                                                           383 RKRVLEMEGKDEEITKTEAQCRELKKKLQEEEHHSKELRLEVEKLQKRMSELEKLEEAFS
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
14.6%; Score 891; DB 4; Length 1046;
Best Local Similarity 31.9%; Pred. No. 1.8e-27;
Matches 283; Conservative 142; Mismatches 303; Indels 160; Gaps
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                                          1046 AA; 116695 MW; 2942129B20048C7F CRC64;
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PROSITE; PS00215; MITOCH_CARRIER; 1.

NON TER 1 1 1 SEQUENCE 1046 AA; 116695 MW; 294;
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957 PNVMSQKPKSADPTLGPERAMSPVTITTISREKSPEGGRSAFADRPASPI----QIMTVS 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 AKLANQE--SHNRQLRLKLVGLSQRIBELEETNKSLQKAEEELQELREKIAKGECGNSSL 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SNMGMGTDS--GTQETKRTEDRFAPGSSHSEG-----KRGREQPSVLS 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----LAPKQGQPLHIRVTPDHENSTATLEITSPTSEEFFSSTTVIPTLGNQKPRITIIPS 956
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                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1101 _ TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ICR;
MEDLINE=96411647; PubMed=8812416;
MEDLINE=96411647; PubMed=8812416;
Sun D.S., Chang A.C., Jenkins N.A., Gilbert D.J., Copeland N.G.,
Chang N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification, molecular characterization, and chromosomal localization of the cDNA encoding a novel leucine zipper motif-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.8%; Score 839; DB 11; Length 1067; Best Local Similarity 29.3%; Pred. No. 2e-25; Matches 275; Conservative 150; Mismatches 326; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:107629; Luzpl.
SEQUENCE 1067 AA; 119289 MW; 381F1C16181749CA CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L49344; AAA98795.1; -. HSSP; P04268; 1IC2.
                                                                                                         Leucine zipper protein 1
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	Search completed: September 7, 2004, 13:16:32	Search completed: S	Se
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746	687 POPNSREKVKSRGGTRTALFENDKNAAIENDSVKPTRPSSNAIEFPDANCAGVKNORPFS 746		엄
1082	1046 PAPVRKYNSNANIITTEDNKIHIHLGSOFKRSPGPAA		δ
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using frame plus n2p model OM nucleic

September 7, 2004, 13:17:40; Search time 403 Seconds (without alignments) 6119.292 Million cell updates/sec Run on:

US-10-788-793-1

Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL-Erame+ n.D.p. model - DEV=x1p
-Q=/cgn2\_1/USFTO\_spool\_p/USIO788793/runat\_07092004\_134020\_10795/app\_query.fasta\_1.4551
-Q=/cgn2\_1/USFTO\_spool\_p/USIO788793/runat\_07092004\_134020\_10795/app\_query.fasta\_1.4551
-DB=A\_Geneseq\_295and+-QFMT=fastan-SUFFTX=rag-MINMATCH=0.1\_LCOPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 -RMD=1 -MATRIX=blosum62 -TRANS=humand+0.cdi
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXEN=200000000
-USER=USI0788793\_@CGN 1 1 642 @runat\_07092004 134020\_10795 -NCFU=6 -ICFU=3
-NO WMAP -LARCEGUERY -NGSE=0 -WARRADS=1 - SCRAPOR=0
-DEV\_TREDUT=120 -WARN TIMBOUT=30 -THREADS=1 - XGAPDEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

geneseqp2000s:\*
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	<u>;</u>		Abp97029 Rat L-FIL	Human pol	Human L-F	Rat S-FIL	Human pro	Human pro	GPBP-inte	GPBP-inte	GPBP-inte	Human CGD
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## ALIGNMENTS

ABP97029 standard; protein; 1212 AA. (first entry) 18-JUN-2003 ABP97029; RESULT 1 ABP9702 

L-FILIP, S-FILIP, filamin-interacting protein; cell migration; cell death; cytostatic; neuroprotective; immunosuppressive; cancer; tumour metastasis; transplantation therapy. Rat L-FILIP protein SEQ ID NO:2.

Rattus norvegicus

WO2003018804-A1.

06-MAR-2003.

29-JUL-2002; 2002WO-JP007676.

(NISC-) JAPAN SCI & TECHNOLOGY CORP. 27-AUG-2001; 2001JP-00256910.

Sato M, Nagano T;

WPI; 2003-268423/26. N-PSDB; ACC45354.

Proteins controlling cell migration and cell death and their encoded DNAs, applicable in developing drugs for treating or suppressing cancer or tumor metastasis or as regulators of cell migration for

 us-10-788-793-1.rag

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GlnAlaArgLysGluLysGluAsnAlaLysArgLeuAsnLysLeuArgAspGluLeuVal
                                                                  GlyLeuGlnSerGlnLysValGlnAspLeuThrGlnLysLeuArgGluGluGluGluLuLys
                                                                                                                                        GCGAATCAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTTGGCTTATCGCAAAGG
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                                 The present sequence represents rat L-FILIP which is a filamin-interacting protein. L-FILIP has a function of controlling cell migration and cell death. L-FILIP has a function not controlling cell migration immunosuppressive activities. The L-FILIP protein can be used for controlling cell migration and cell death, which is applicable in developing drugs for treating or suppressing cancer or tumour metastasis or as regulators of cell migration for transplantation therapy, and also for controlling the mobility and cell death of inerve cells, promoting protein in the treatment of preiventrilcular nodular heterotopia
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                                                                     CAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAG
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AGGCCTGCATCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATC 1081 AlaAlaGluGlyValSerProVallleThrValArg9roValAsnValThrAlaGluLys cancer; CNS; ACGATTACTACTATTTCCAGAGAGAGAGCCCCGGAAGGTGGAAGGAGCGCCTTTGCCGAC ThrileThrThrileSerArgGluLysSerProGluGlyGlyArgSerAlaPheAlaAsp GCTGTCTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCG GAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACC GCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAG GluValSerThrGlyThrValLeuArgSerProArgAsnHisLeuSerSerArgProGly GCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTCACAACGTCATCCACGAGGA AlaSerLysValThrSerThr1leThr1leThrProValThrThrSerSerThrArgGly ATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAATCTG SerGlnLygProLygSerAlaAspProThrLeuGlyProGluArgAlaMetSerProVal GAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGGAACCACCTCTCTTCAAGACCCGGT ACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCCGCATTCCT Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; CNS; plathaimer's; Parkinson's disease; Huntington's disease; handraic; Alzhaimer's; Parkinson's disease; Huntington's disease; hamostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; GCCAGCAGCACTGCTCTTGGAGGGGGGAAGGGC Ş Human polypeptide SEQ ID NO 3161.

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731 220 791 240 851

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81 IleGlnLeuLeuSerIleMetGluGlyGluLeuGlnAlaArgGluAsgValIleHisMet 100
                                                                        141 GluAspValTyrGluLysProileSerGluLeuAspArgLeuGluGluLysGlu 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAAI871394). The polyprocessant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system—such as Deribheral nervous system—such as Deribheral nervous system—such as Deribheral nervous system—such as Deribheral nervous system—such as Deribheral nervous system—such as Deribheral nervous system diseases, Buch as localised neuropathies and Central nervous system diseases, Buch as Alzhelmer F. Perrinnon's disease. Huntingcon a Grasser and Central as Alzhelmer and central nervous system suppression, attain of the activities such as Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S. disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                   Wang D;
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                                                                                                                                                                                                                                                                                                                                                             vel nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.
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                                                                     25-APR-2000; 2000US-00488725.
25-APR-2000; 2000US-00488725.
20-UTN-2000; 2000US-00588042.
19-UUL-2000; 2000US-00588042.
03-AUG-2000; 2000US-00683450.
14-SEP-2000; 2000US-00663191.
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29-NOV-2000; 2000US-00727344.
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TCCACTCCGCAGGAGAAAGGGCCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGAGCTG GTCCTAGCACCAAAGCAGGGCCAGCCCCTACACATCCGTGTGACACCCAGATCATCAGAAC ACCACGGAAGACAATAAAATTCACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGG ThrThrGluAspAsnLysIleHisIleHisLeuGlySerGlnPheLysArgSerProGly

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Page 6

135 TCCTCCATCATCAGGAGTGATGATGGTAAGGCCCCTCAGAAGAGGAC 191	y 252 CCATCTGCAGAAAAGTCAAAAAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTC 311	y 312 ATCCAGCTCCTGAGTATCATGGAAGGGGGTGTTGCAGGGTCGAGAAGATGTCATCCACATG 371	y 372 CTGAGGACAGAGACCAAGCCCGAGGTTCTGGAGGCACACTATGGATCTGCAGAACCT 431    :::	432 GAGAAAGIGCTICGGGICCTGCACGAGATGCCATCCTTGCTCAAGAGAAGTCCATAGGA 491	492 GAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGAAAAGCAGAAGGAG 551	552 ACGTACCGCCGCATGCTAGAGCAGCTGCTGGCTGAGAAGTGTCACAGGGGCGCACCGTG 	612 TACGAGGGAGAACGAGAAGCACACTGACTACATGAACAAGAGGACACTTC	672 ACCAACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	201 732 221	792 GTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGACGAGGAGGCAGATGCACATCGAGCAA 851	852 CTGGGCCTGCAGAAGTCCAGACCTCACTCAGAGCTGAGGAGGAGGAGAAGAAGA	912	972 GTGGACTTCGAACACACAGGGTTTTCCCAGGAGCACGAAGATGAACGCCAA 1031 	1032 TTGGCGAATCAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTTGGCTTATCGCAA 1091 	1092 AGGATTGAGGAGGTGGAAGACCAATAAAAGCCTTCAGAAGGGAGAAGAGGTCCAG 1151 	1152 GAGCTGAGAGAAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTG 1211
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	RESULT 3 ARP97031 ID ABP97031 standard; protein; 1213 AA. XX	AC ABP97031; XX DT 18-JUN-2003 (first entry) XX	Human L-FILIP protein SEQ ID NO:6.  L-FILIP, S-FILIP, filamin-interacting protein; cell migratio		PN WO2003018804-A1. XX PD 06-MAR-2003.	PP 29-JUL-2002; 2002MO-JP007676. XX PR 27-AUG-2001; 2001JP-00256910.	XX PI Sato M, Nagano T;	XX DR WPI; 2003-268423/26. DR N-PSDB; ACC45356.	XX Proteins controlling cell migration and cell death and their encoded Pr DNAs, applicable in developing drugs for treating or suppressing cancer Pr or tumor metastasis or as regulators of cell migration for Pr transplantation.		CC interacting protein. L-FiliP has a function of controlling cell migration can death. L-FiliP has cytostatic, neuroprotective and cell migration act immunosuppressive activities. The L-FiliP protein can be used for CC controlling cell migration and cell death, which is applicable in		XX SQ Sequence 1213 AA;	Pred. No.: 0 Length: 1213 Score: 5696.50 Matches: 1134 Percent Similarity: 96.54 Conservative: 37 Best Local Similarity: 93.49\$ Mismarches: 41	73.68% Indels: 6 Gaps: 64 × ARDOGANT (1-1012)	OY 75 ATGAGATCACGAAAAAAGTTCATCTAACGGGCATGTCTCCTGCCCCAAG 134

11   LeuSerGinLeudinValNapTyrSerValLeuGinGinArgheHetGiuGiudhann 760
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Qy 3432 GGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCGGTC	ACAACGICAICCACACGA 3491	Score:
Db 1121 GlyAlaSerLysValThrSerThrIleThrIleThrProValThrThrSerAlaArg		Best Loc
Qy 3492 GGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCGCATT	CCTACCCCACCCCATT 3551	Query Ma
Db 1141 GlyThrGlnSerValSerGlyGlnAspGlySerSerGlnArgProThrProThrArglle		US-10-78
Qy 3552 CCTATGTCAAAAGGTATGAAAGCTGGAAAAGCCAGTAGTGGCAGCAGGAGCAGGAATT	GCCTCAGGAGCAGGAAAT 3611	γo
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Db 1201 AlaAlaSerSerThrThrSerLeuGlyGlyGlyLysGly 1213	13	QQ
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<pre>ID ABP97030 standard; protein; 965 AA. XX</pre>		qa
AC ABP97030; XX		ζö
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DE Rat S-FILIP protein SEQ ID NO:4.		ờ
KW L-FILIP, S-FILIP, filamin-interacting protein, cell migration, KW cell death, cytostatic; neuroprotetive; immunosuppressive; cancer; KW tumming metaetagis. Francolaries of the concer;	migration; ressive; cancer;	<b>q</b> .
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I Sato M, Nagano T;		qa
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T DNAs, applicable in developing drugs for treating or suppressing can T or tumor metastasis or as regulators of cell migration for T transplantation.	r suppressing cancer ion for	yo du
X S Claim 4; Page 68-73; 96pp; Japanese.		8
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C. or as regulators of cell migration for transplantation therapy, and also for controlling the mobility and cell dash of news cells.	or therapy, and also	ð
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221 GluLeuGluValValLysSerArgValLysGluLeuGluCysSerGluSerArgLeuGlu
                                                                             1416 TGCACCCAGCTCCATCTGAACCTGGAGAAGGAGAAGAACCTAACCAAAGACCTGCTGAAC
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IleMetThrValSerThrSerAlaAlaProThrGluIleAlaValSerProGluSerGln GATCCTACTCCGCCCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGA GAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCATCCCCATCCAA GTTATCACCGTCCGGCCTGTCAACGTGACAGGGAGAAGGAGGTTTCTACAGGCACAGTC ATAACTATAACCCCGGTCACAACGTCATCCACACGAGGAACCCAATCAGTGTCAGGACAA ATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCA detection; diagnosis; antisense therapy; gene therapy

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CC length cDNAs defined in the specification. Where a primer set comprises:

CC an oligo-dT primer and an oligomucleotide comprimentary to the complementary strand of a polynucleotide which comprises one of the 5602 culleotide sequences defined in the specification, where the oligomucleotide comprises at least 15 nucleotides; or (b) a combination of an oligomucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligomucleotide comprising a sequence complementary to the oplynucleotide which comprises a 3'-end sequence, where the oligomucleotide which comprises a 3'-end sequence, where the oligomucleotide which comprises a 3'-end sequence, where the oligomucleotide sequence 3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers sets can be used in antisense therapy and in generication and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the ANH13613 to ANH18613 to ANH18613 to ANH18613 to ANH18613 to ANH18613 to Papersent human amino acid sequences; and ANH1862 to ANH1362 represent coligomucleotides, all of which are used in the exemplification of the protein of the protein of the protein of the protein of the protein of the protein of the coligomucleotides, all of which are used in the exemplification of the protein of the coligomucleotides.
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                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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Otsuki T;
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27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-NAXY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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                                                                                                        AAGGAGGTTTCTACAGGCACAGTCCTTCGCTCTCCCAGGAACCACCTCTTCAAGACCC 3431
                                                 3132 ATCGCTGTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACC 3191
                                                                                                                                      CCTGCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGGGGAG 3371
                                                                                                                                                                                              GGTGCTAGCAAAGTGACCAGCACTATAACTATAACCCCGGTCACAACGTCATCCACACGA 3491
                                                                                                                                                                                                                            GGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCCGCATT 3551
                                                                                                                                                                                                                                                        CCTATGTCAAAAGGTATGAAAGCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAAT 3611
                                                                                                                                                                                                                                                                                    CTGACCAAATTCCAGCCTCGAGCTGAGACTCAGTCTATGAAAATAGAGCTGAAGAAATCT 3671
                                                                              CCGGAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATC 3251
521 ThrSerGlyGluGlyValSerProVallleThrValArgProValAsnValThrAlaGlu 540
                                                                                                                                                                            601 ProMetSerLysGlyMetLysAlaGlyLysProValValAlaAlaProGlyAlaGlyAsn 620
                                                                                                                                                                                                                                    IleAlaValSerProGluSerGlnGluMetProMetGlyAkgThrIleLeuLy8ValThr
                     GACAGGCCTGCATCCCCATCCAAATCATGACGGTGTCAACATCTGCAGCTCCCACTGAA
                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                 GCAGCCAGCACTGCCTCTTGGAGGGGGGAAGGGC 3710
                                                                                                                                                                                                                                                                                                                         641 AlaAlaSerSerThrThrSerLeuGlyGlyGlyLysGly
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11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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The present invention describes primer sets for synthesising 5602 full-

[a] an Oligo-dr primer and an oligonucleotide complementary to the

[c] an oligo-dr primer and an oligonucleotide complementary to the

[c] complementary strand of a polynucleotide which comprises one of the 5602

[c] connoid-sotide comprises at least 15 nucleotides; or (b) a combination

[c] connoid-sotide comprises at least 15 nucleotides; or (b) a combination

[c] connoid-sotide comprises a sequence complementary to the

[c] conplementary strand of a polynucleotide which comprises a 5'-end

[c] conplementary strand of a polynucleotide which comprises a 5'-end

[c] conplementary strand of a polynucleotide which complementary to a

[c] conplementary strand of a polynucleotide which complementary to a

[c] conplementary strand of a polynucleotide which complementary to a

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[c] conplementary strand of a polynucleotide on the complementary to a

[c] conplementary strand of a polynucleotide on the complementary to a

[c] conplementary strand of the abnormality of the proteins encoded by

[c] contain and confident on the primers are also useful for the full-length

[c] contains easily without any specialised methods. AAH03165 to AAH13628 represent

[c] contains and add sequences, and AAH13632 to AAH13632 represent

[c] contains and cold sequences and the exemplification of the

[c] contains and cold sequences and the exemplification of the
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                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
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                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID NO 12253; 2537pp + Sequence Listing; English.
   Saito K,
Otsuki
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Mismatches:
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oggai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
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   Isogai T,
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The present sequence is the protein sequence of GIP130b, a novel 130 kDa Goodpasture antigen binding protein (GPBP) interacting protein. The DOC/GIP90/130 mRNA family results from a complex diversification mechanism operating on the expression of the GIP90 gene on chromosome 3 (3q12). GIP90/130 polypeptides of the invention interact with GPBP and are capable of aggregation. They can be used to modify GPBP-GIP90/130 interactions, to modify GP90/130 aggregation, and to modify GPBP-GIP90/130 interactions, to modify GP90/130 aggregation, and to modulate gene expression. The invention provides GIP90/130 polypeptides, portions of them, antibodies, nucleic acid sequences, expression vectors and host cells, as well as methods for detecting GIP90/130 polypeptides and nucleic acids, and methods for treating an autoimmune disease or cancer by modifying the expression or activity of one or more GIP90/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                Goodpasture antigen binding protein interacting protein; GPBP; GIP130b; human; transcription factor; autoimmune disease; cancer; immunosuppressive; cytostatic.
501 SerValLeuGlnGlnArgPheMetGluGluGluAsnLysAsnLysAsnMetGlyGlnGlu
                                                    1133
                                                                                                                                                                                             AGTGGGAACGCCCGAAGGATGGTGGACGTG 2465
                                                                                                                                                                                                                   Claim 8; Page 78-83; 115pp; English.
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20-MAY-2002; 2002US-0382004P.
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(REVE/) REVERT-ROS F.
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N-PSDB; ACC83929.
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27-20	•	ABR62232 (1-11	-1133)				õ	1140
දු දු	/5 ATGAGATCACGA             1 MetArgSerArg		AAGTTCATCTAACG :::: oThrGluGlySerA	AISAAAICACGAAAICAAGGIGGAGAAATICAICIAACGGGGAIGICTCCIGCCCCAAG 	AG 134 :: 18		qq	349
Š		LOCACOLACHDA OBA OLA.	Death and the second se	CTCTCTTCTTCTTCTTCTTCTTTTTTTTTTTTTTTTTT			δ	1200
g G	າ ຫ	199199199199999		GIMGGGCCCCCICAGAGGAIGCAAAAAAAAAAAAAAAAAA			Ob	369
ò	L LO	AAGGAGGAGGATGTC	PATGGGTTGGGAA	GCCAATCGGAAGGAGGAGGATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA			λŏ	1260
; 名		LysHisArgGlnGlnAspLysAspSerProSerGluSerAspVal	::: ProSerGluSerA	s:: spvallleLeu			Д	389
ò	252 CCATCTGGA	CCATCTGGAGAAGTGAGAAA	AAGACTA	AGAAGTCTGTGGAGTTATC	CC 299		ò	1320
οg		::::::       LysAlaGluLysProHie	SerGlyAsnGlyH	 ProCysProLysAlaGluLysProHisSerGlyAsnGlyHisGlnAlaGluAspLeuSer	— н		Db	409
δ	300 AAGGAGGAC	CTCATCCAGCTCCTGAGI	ATCATGGAAGGG	AAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGAAGAT			λΌ	1380
QQ	:::::     69 ArgAspAsp	:::	:::       :1leLeuGluGlyG	:::::        :::			QQ	429
ò	360 GTCATCCAC	ATGCTGAGGACAGAAA	ACCAAGCCCGAGG	GTCATCCACATGCTGAGGACAGAGAAACCAAGCCCGAGGTTCTGGAGGCACACTATGGA	3A 419		λō	1440
q		:::   :::         TleLeuLysAlaGluLys	: MetAspLeuAlaL	:::   :::			Op Q	449
λŏ	420 TCTGCAGAA	CCTGAGAAAGTGCTTCGG	GTCCTGCACCGAG	TCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACGAGATGCCATCCTTGCTCAAGAG	4G 479		à	1500
q	109 PheValThr	:::         ProLysLysValLeuGlu	 	:::	er 128		qq	469
ò	480 AAGTCCATA	GGAGAAGACGTCTATGAC	AAACCTATCTCAG	AAGTCCATAGGAGAGGCTCTATGAGAAACCTATCTCAGAGCTGGACAGGCTGGAGGAA	4A 539		λ̈́o	1560
οp	129 ThrProTrp	:::         GlnGluAspIleTyrGlu	  LysProMetAsnG	ThrProTrpGlnGluAspIleTyrGluLysProMetAsnGluLeuAspLysValValGlu	  u 148		QD .	489
ò	540 AAGCAGAAG	igagaceracicececare	cragascascrec	TGCTGGCTGAGAAGTGTC	AÇ 599		٥٨ م	1620
Ор	  149 LysHisLys	:::        :::  GluSerTyrArgArgIle	  LeuGlyGlnLeuL	:::	-  s 168		q	509
ò	600 AGGCGCACC	GTGTACGAGCTGGAGAAC	GAGAAGCACAAGC	GGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACCTGACTACATGAACAAG	4G 659		à	1680
q	:::    169 ArgGlnThr	:::          TleLeuGluLeuGluGlu	  GluLysArgLysH	:::   :::   ArgGlnThrIleLeuGluLeuGluGluGluLysArgLysHisLysGluTyrMetGluLys			DÞ	529
ò	660 AGCGACGAC	TTCACCAACCTGCTGGAG	CAGGAGCGAGAGA	GCGACGACTTCACCAACCTGGAGCAGGAGCGAGAGGAGGTTGAAAAAGCTCCTTGAA	4A 719		à	1740
qq	::: 189 SerAspGlu	  PhelleCysLeuLeuGlu	          GlnGluCysGluA	:::    erAspGluPheIleCysLeuLeuGluGlnGluCysGluArgLeuLysLysLysLeuIleAsp	20		QQ	549
ò	720 CAAGAAAAA	GCTTACCAAGCCCGCAAA	GAAAAGGAAAACG	CAAGAAAAGCTTACCAAGCCGGAAAGAAAAGGAAAAGGTAAAGGGGCTCAACAACTT	779		ò	1800
qq	209 GlnGluile	   LysSerGinGluGluLys	:::    GluGlnGluLysG	  GinGluileLysSerGinGluGluLysGluGluGluLysGluLysArgValThrThrLeu	 su 228		qo ,	569
ò	780 CGAGATGAG	crrereaagcrcaagrc	Treecercarer	TGGTGGACGAGAGGCAGAT	rg 839		ò	1860
С	229 LysGluGlu	  LeuThrLysLeuLysSer		::::::	rg 248		qq	589
ò	840 CACATCGAG	CAACTGGGCCTGCAGAGT	CAGAAAGTCCAGG	CACATCGAGCAACTGGGCCTGCAGAGTCAGAAAGTCCAGGACCTCACTCA	9G 899		λ	1914
qa	249 LeuThrAla	  GlnLeuThrLeuGlnArg	:::   : GlnLysIleGlnG		: : 78 268		qa 🛴	609
ò	900 GAGGAGGAA	GAAAAÇTÇAAAGCGGTC	ACTTACAAATCCA	GAGGAGGAAGAAAGTCAAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTG	rg 959		à	1968
qq	 269 GluThrHis'	 ThrLysLeuAlaLeuAla	::: :: GluAlaArgValG		la 288		q <sub>O</sub>	629
ο̈́λ	960 CTCAAGTTA	GAAGTGGACTTCGAACAC	AAGGCCTCGAGGT	CTCAAGTTAGAAGTGGACTTCGAACACAAGGCCTCGAGGGTTTTTCCCAGGAGCACGAAGAG	4G 1019	·	ò t	2028
qa	289 ThrArgLeu	  GluLysGluLeuGlnThr	GlnThrThrLysP	ThrargleugluLysgluLeuglnThrdlnThrThrLysPheHisGlnAspGlnAspThr	ır 308		2 2	64.9
ò	1020 ATGAACGCC	aaattggcgaatcaagaa	TCTCACAACCGGC	atgaacgccaaattggcgaatcaagaatctcacaaccggcaacttcgactcaaactggtt	T, 1079	—.·		0 0 0 0 0

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CACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCAGTT 3338
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LysThr-----ThrAsnLysValThrSerSerIle 1111
                                                                                                                                                                                                                                                                                  SerProSerAlaProLeuGlnAspAsnArgThrGlnGlyLeuIleAsnGlyAlaLeuAsn 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the protein sequence of GIP130c, a novel 130 kDa Goodpasture antigen binding protein (GPBP) interacting protein. The DDC/GIP190/130 mRNA family results from a complex diversification mechanism operating on the expression of the GIP90 gene on chromosome 3 (3q12). GIP90/130 polypeptides of the invention interact with GPBP and are capable of aggregation. They can be used to modify GPBP-GIP90/130 interactions, to modify GP90/130 aggregation, and to modulate gene expression. The invention provides GIP90/130 polypeptides, portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goodpasture antigen binding protein interacting protein; GPBP; GIP130c; human; transcription factor; autoimmune disease; cancer; immunosuppressive; cytostatic.
                                                                                                                 :::
IleSerAlaLysHisAlaIlePheArgValSerProAspArgGlnSerSerTrpGlnPhe
                                                                                                                                                                                                                                                                                                                            CGCTCTCCCAGGAACCACCTCTCTTCAAGACCCGGTGCTAGCAAAGTGACCAGCACTATA
                                                                                          GTGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGACAATAAAATTCACATT
                                                                                                                                                                                                                                                                                                                                                                                                      ACTATAACCCCGGTCACAACGTCATCCACACGAGGAACCCAA 3500
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20-MAY-2002; 2002US-0382004P.
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LysAlaGlnPheLeuSerLysGluLeuGluHisValLysMetGluLeuAlaLysTyrLys 688
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788 ArgArgIleSerAspProGlnValPheSerLysGluValGlnThrGluAlaVal-----
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                                                                                                                                                                                         ThrProTrpGlnGluAspIleTyrGluLysProMetAsnGluLeuAspLysValValGlu
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3158 1024 3039 AAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCATCCCCATCCAAATC 3098 CACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCAGTT 3338 3399 CGCTCTCCCAGGAACCACCTCTCTTCAAGACCCGGTGCTAGCAAAGTGACCAGCACTATA 3458 New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or Goodpasture antigen binding protein interacting protein; GPBP; GIP130a; human; transcription factor; autoimmune disease; cancer; immunosuppressive; cytostatic. GlnThrProGluSerCysGlySerLeuThrProGluArgThrMetSerProIleGlnVal ATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCGAATCTCTCAGGAA ::: IleSerAlaLysHisAlaIlePheArgValSerProAspArgGlnSerSerTrpGlnPhe 3339 ATCACCGTCCGGCCTGTCAACGTGACAGGGAGAAGGAGGTTTCTACAGGCACAGTCCTT 1082 SerProSerAlaProLeuGlnAspAsnArgThrGlnGlyLeuIleAsnGlyAlaLeuAsn GIGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGACAATAAAATTCACATT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of GIP130a, a novel 130 kDa Goodpasture antigen binding protein (GPBP) interacting protein. GIP130a cDNA was isolated from a skeletal muscle cDNA library. It represents an mRNA species that results from faithful transcription and translation of GIP90 genomic DNA. GIP90/130 polypeptides interact with GPBP and are GIP90 genomic DNA. GIP90/130 polypeptides interact with GPBP and are interactions, to modify GP90/130 agregation, and to modulate gene expression. The invention provides GIP90/130 polypeptides, portions of them, antibodies, nucleic acid sequences, expression vectors and host cells, as well as methods for tecting GIP90/130 polypeptides and nucleic acids, and methods for treating an autoimmune disease or cancer by modifying the expression or activity of one or more GIP90/130
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|ProCysProLysAlaGluLysProHisSerGlyAsnGlyHisGlnAlaGluAspLeuSer
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Claim 7; Page 68-72; 115pp; English
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The invention relates to an isolated polypeptide associated with cell growth, differentiation and death (CGDD). Also disclosed are the polyperides encoding the polypeptides. The polypeptides and polymucleotides are useful in disquestive. The polypeptides and preventing diseases or conditions associated with the decreased expression or expression of CGDD. Such diseases include cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatcry (e.g. AIDS, allergies) and reproductive disorders, or disorders of the placenta. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of CGDD. The CGDD or its fragments are useful in screening compounds for effectiveness as an of nucleic and amino acid sequences of CGDD. The CGDD or its fragments are useful in screening compounds that specifically bind to or modulate the activity of the polypeptide. Microarrays consisting polymucleotides of the invention are useful in monitoring or measuring expression profiles. Sequences given in records AAR69667 represent CGDD polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  996 AGGITITCCCAGGAGCACGAAGAGATGAACGCCAAATTGGCGAATCAAGAATCTCACAAC 1055
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|GlnGluLeuThrThrAsnAlaLysGluThrHisThrLysLeuAlaLeuAlaGluAlaArg
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                                                  09-NOV-2001; 2001US-0344518P.
09-NOV-2001; 2001US-0345143P.
16-NOV-2001; 2001US-0332375P.
03-DEC-2001; 2001US-0336908P.
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26-OCT-2001;
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                                                                                                                                                                  New Goodpasture antigen binding protein-interacting 90 and 130 kDa polypeptides, useful for diagnosing and/or treating disorders associated with the GIP90/130 polypeptide, such as autoimmune disorders and/or
                          3135 GCTGTCTCTCCTGAATCTCAGGAAGTGCCTATGGGAAGGACTATCCTCAAAGTCACCCCGG
                                                          GAAAAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACC
                                                                         3315 GCCGCTGAAGGCGTGAGCCCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAG
                                                                                                        ACGGBAGACAATAAAATTCACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCT
                                                                                                                                                                                                              ::: ||| :: :: ||| 854 GlyLeuIleAsnGlyAlaLeuAsnLysThr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodpasture antigen binding protein interacting protein; GPBP; GIP90; human; transcription factor; autoimmune disease; cancer; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the protein sequence of GIP90, a novel 90 kDa doodpasture antigen binding protein (GPBP) interacting protein. GIP90 CDMA was isolated following a yeast two-hybrid screen for GPBP interactive proteins and use of a partial clone to screen a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 59-62; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GPBP-interacting protein GIP90
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20-MAY-2002; 2002US-0382004P.
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                                                                                                                2244 CAGGCTCTCAAGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTC 2303
                                                                                                                                                             2304 CAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAAAGTAAGAACTAAGAACAAGAAAC 2363
                                                                                                                                                                                                                                                                                                                                                ------GCTGTGTTCATTCGCAAATCCTTCCAGGAG---GAAAATCAC 2570
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                                                                                                                                                                                                                                                                                                                                                                                                                    606 SerPheLysCysSerGlnSerThrProCysProValAsn------ArgLysLeu 621
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LysMetGluLeuAlaLysTyrLysLeuAlaGluLysThrGlu---ThrSerHisGluGln
                                                                                                                                  480 AspAlaLeuLysGluLysIleHisGluTyrMetAlaThrGluAspLeuIleCysHisLeu
                                                                                                                                                                            GCTCTCAGGCCGAGTGGGAACGCCCGAAGGATGGTGGACGTGCCTGTGGCCTTCACTGGG
                                                                  2184 GAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTG
                                                                                    GTGCAGACCGAGCGGTGTGCGGGGATGCTGCGGAGGAGGAGACCCCG------
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skeletal muscle cDNA library. The GIP90 gene was localised to chromosome existence of an adenine at position 2720 in the cDNA that was not present in GIP90 genomic DNA. Another CDNA fragment was isolated that was not present in GIP90 genomic DNA. Another CDNA fragment was isolated that encoded a LIO kDa protein (GIP100, see ABR6221) and resulted from faithful transcription and translation of the GIP90 genomic sequence (i.e. no AZ720). GIP90/130 polypeptides interact with GPBP and are capable of modify GP90/130 aggregation, and to modify GPBP-GIP90/130 interactions, to modify GP90/130 aggregation, and to modulate gene expression. The invention provides GIP90/130 polypeptides, portions of them, antibodies, mucleic acid sequences, expression vectors and host cells, as well as methods for detecting GIP90/130 polypeptides and nucleic acids, and methods for treating an autochmune disease or cancer by modifying the expression or activity of one or more GIP90/130 polypeptides 

Š Sequence 764

TCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTTGCTCAAGAG 479 ThrProTrpGlnGluAspIleTyrGluLysProMetAsnGluLeuAspLysValValGlu 148 AAGGAGGACCTCATCCAGCTCCTGAGTATCATGGAAGGGGAGTTGCAGGCTCGAGAAGAT 359 ATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCTAACGGGCATGTCTCCTGCCCCAAG 134 GCCAATCGGAAGGAGGAG---GATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA 251 PheValThrProLysLysValLeuGluAlaLeuGlnArgAspAlaPheGlnAlaLysSer 135 TCCTCCATCATCAGCAGTGATGGTGGTAAGGGCCCCTCAGAAGAAGAAGAAGAACAAG HisThr------ysGlyHisSerPheGlnGlyProLysAsnMet CCATCTGGAGAAAGTGAGAAA------AAGACTAAGAAGTCTGTGGAGTTATCC ||| | ProCysProLysAlaGluLysProHisSerGlyAsnGlyHisGlnAlaGluAspLeuSer GTCATCCACATGCTGAGGACAGAAAACCAAGCCCGAGGTTCTGGAGGCACACTATGGA AAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGACTGGAGGAA 764 386 1144 2210 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-764)US-10-788-793-1 (1-4364) x ABR62250 2.23e-115 1828.00 69.55% 50.66% 23.65% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 75 -19 195 252 300 83 120 109 890 129 32 49 69 360 Query Match: DB: 셤 ò 6 6 6 8 4 8 6 8 6 8 6 8 8 6 8 6

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AGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACTGACTACATGAACAAG

AGCGACGACTTCACCAACCTGCTGGAGCAGGAGCGAGAGGTTGAAAAAGCTCCTTGAA 719 |||||||:::||| |SerAspGluPheIleCysLeuLeuGluGluGluCysGluArgLeuLysLysLeuIleAsp 208 CAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAACGCTAAAGCGGCTCAACAAACTT 779

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1079 1139 1259 1319 1439 1499 1559 1619 1679 1739 1859 960 CTCAAGTTAGAAGTGGACTTCGAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAG 1019 GAAGAGCTCCAGGAGCTGAGAGAGAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTC 1199 488 CTCAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGGGGATGAGGTGATG 1799 248 348 408 448 528 588 329 AlaLeuSerArgGlnIleAspGluLeuGluGluThrAsnArgSerLeuArgLysAlaGlu ||||||||||||||:::::::|||||||||::: ::: |GluGluLeuGlnAspIleLysGluLysIleSerLysGlyGluTyrGlyAsnAlaGlyIle ATCACGAAGACCGAGGCCCAGTGCCGGGAGCTGAAGAAGAAGCTCCAAGAGGAAGAACAC GTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGTTAAGCCTCAAAGAT GACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGGAAAAAAATATGATG GlnGluIleLysSerGlnGluGluLysGluGlnGluLysGluLysArgValThrLeu GAGGAGGAAGAAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTG 1020 ATGAACGCCAAATTGGCGAATCAAAGAATCTCACAACCGGCAACTTCGACTCAAACTGGTT 1080 GGCTTATCGCAAAGGATTGAGGAGCTGGAAGAGCCAATAAAAGCCTTCAGAAGGCAGAG CACAGCAAGGAACTTAGACTAGAAGTGGAGAGCTGCAGAAGAGGATGTCTGAGCTGGAG AAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTGAACCTG GAGAAGGAGAAGCTAACCAAAGACCTGCTGAACGAGCTGGAGGTGAAGAGTCGA |||||||||:: |SluLysGluArgMetThrThrLysGlnLeuSerGlnGluLeuGluSerLeuLysValArg GAGAAAATAAAGCAAGAAGAGGAAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAG |||||||:::|||::: |GluLysLeuLysLysThrGluAspLysLeuGlnAlaAlaSerSerGlnLeuGlnValGlu CAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAAGCAAGAAGCTTTTAAAA GGTAAACTGAGGAGCGAAGAAGAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTA 289 309 1140 1260 209 780 229 840 249 900 269 349 389 1320 409 1380 429 1440 449 1500 1560 489 1620 509 1680 529 1740 1800 569 g g ò g ò 원 유 g ò g 요 g ò ò ò ò 8 ઠ ò 셤 à ద δ 셤 ð g ઠે 원장 g 8 8 8 원 8 셤

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                                           The present sequence is that of a 785-amino acid polypeptide that is present in the movel Goodpasture antigen binding protein (GPBP) interacting protein GIPPJO (GREP ABR62251). The polypeptide lacks critical regions of GIP90/130 polypeptides implicated in GPBP interaction and induction of gene expression, but contains sequences that downerequate interaction with GPBP. The polypeptide, or antibodies to it, can be used to modify GPBP-GIP90/130 polypeptide interactions or to modify GPBP-GIP90/130 polypeptides proteins of them, antibodies, mucleic acid sequences, expression vectors and host cells, as well as methods for detecting GIP90/130 polypeptides and nucleic acids, and methods for treating an autoimmune disease or cancer by modifying the expression or activity of one or more GIP90/130 polypeptides
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LysvalThrThrValThrGluLysLeuIleGluGluThrLysArgAlaLeuLysSerLys
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|GluArgMetThrThrLysGlnLeuSerGlnGluLeuGluSerLeuLysValArgIleLys
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                        Claim 34; Page 102-106; 115pp; English.
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                  ACGCTTGAAATCGAGAGACTGAAAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGAC 2027
                                                                                                                                                                                                                     648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodpasture antigen binding protein interacting protein; GPBP; GIP130a; human; transcription factor; autoimmune disease; cancer; immunosuppressive; cytostatic.
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                                                                                                                                  -----TCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGAACTA
             AAGAAGCGCCTTGATGGCATAGAGGAGGTAGAAAGGGAAATAAACCGAGGTAGG----
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20-MAY-2002; 2002US-0382004P.
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(REVE/) REVERT-ROS F.
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N-PSDB; ACC83934.
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3045 CCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCATCCCGATCCATGACG 3104
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2814 ACACCAGATCATGAGAACAGCACTGCCACCTGGAGATCACAAGCCCCACATCTGAA--- 2870
                                                                                             2928 ACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCCAAA---AGTGCCAGATCCTACT 2984
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               577 ProHisSerTyrThrSerThrAlaVallleProAsnCysGlyThrProLysGlnArglle 596
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| 657 ValThrGlySerAlaSerSerProGluGlnGlyArgSerProGluProThrGluIleSer 676
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597 ThrIleLeuGlnAsnAlaSerIleThrProValLysSerLysThrSerThrGluAspLeu
                                                ---GAGTITITICICIAGIACCACCGICATICCIACCITAGGCAACCAGAAAAA
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| ThrProThrAlaThrProLeuProArgGlnSerGln 775
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The present invention relates to a method for diagnosing breast cancer in a subject suppercted of having endomerizal cancer. The method comprises determining the expression of a set of human genes or expression products in an endomerizal sample suspected of being cancerous. The human genes of the invention are differentially expressed in breast tumours characterised as high or low MAI (mitotic activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products. The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimes, and identification of compounds useful for the treatment regimes, and identification of compounds useful for the treatment of endometrial cancer. MAUS4361 represent the human proteins of the invention that are differentially expressed in breast cancer tissue Diagnosing breast cancer comprises determining expression of nucleic a motecules or expression products that are differentially expressed in normal and malignant tissue. Claim 37; Page 141-143; 219pp; English WPI; 2002-180084/23. N-PSDB; ABK35549. 

Sequence 752 AA

Alignment Score Pred. No.: Scorer Scorer Best Local Similar Best Local		t Scores: 5.57e-103 Length: 752 .: 1645.50 Matches: 363 Similarity: 64.16\$ Conservative: 140 al Similarity: 46.30\$ Mismatches: 216 .tch: 5 Gaps: 13	193-1 (1-4364) x AAU84329 (1-752)	STGGACGAG	1 MetValValAspGluGlnGlnArgLeuThrAlaGlnLeuThrLeuGlnArgGlnLySIle 20	876 CAGGACCTCACTCAGAAGCTGAGGGAGGAGGAAGAAAACTCAAAGCGGTCACTTACAAA 935	21 GlnGluLeuThrThrAsnAlaLysGluThrHisThrLysLeuAlaLeuAlaGluAlaArg 40	CGCCAGAAGCTGCTC	41 ValGlnGluGluGluGlnLysAlaThrArgLeuGluLysGluLeuGlnThrGlnThrThr 60	996 AGGITITCCCAGGAGCACGAAGAGAGGAGGACGAAATIGGCGAATCAAGAATCTCACAAA 1055	61 LysPheHisGlnAspGlnAspThrIleMetAlaLysLeuThrAsnGluAspSerGlnAsn 80	1056 CGGCAACTTCGACTCGAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAAGAACC 1115		1116 AATAAAAGCCTTCAGAAGGCAGAGGAGAGCTCCAGGAGCTGAGAGAAAATTGCCAAA 1175	ysalaglugluLeuGlnAspIleLysGluLysIle	1176 GGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAGAGTCTGCGCAAGCGCGTGCTT 1235	121 GlyGluTyrGlyAsnAlaGlyIleMetAlaGluVal 132	1236 GAGATGGAGGCAAGGATGAAGAGATCACGAAGACCGAGGCCCAGTGCCGGGAGCTGAAG 1295	133GlugluLeurleLysMetGlugluGluCysArgAspLeuAsn 146	1296 AAGAAGCTCCAAGGAAGAACACCACAGCAAGGAACTTAGACTAGAAGTGGAGAAGCTG 1355
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1535 1715 1835 2243 2303 2363 1415 1475 AAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTG 1595 1655 1895 GAAGACAATAAGATCAGAGAACTAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAG 2003 2004 CAGTIGGAGGIGGIGGAGGGGGACTIGAIGACCCGAGGACGAAIAIGACCAGTIGGAG 2063 2064 CAGAAGTICAGAACCGAGCAGGATAAGGCAAACTICCTCTCCCAGCAGCAGGAAATC 2123 2124 AAACACCAAATGGCCAAGCACAAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCC 2183 ATGGGGAGGGAGGTCCTCAATCTGACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGA 2423 GAAATAAACCGAGGTAGG-----TCGTGCAAGGGGTCTGAGTTCACCTGCCCG 1943 266 326 346 445 485 226 ::: ::: ::: 347 AspPheLeulysAsnLysLeuAsnGlnAspSerGlyLysSerThrThrAlaLeuHisGln 366 |||:::|||||||||:::||||||::: |GluAsnAsnLysIleLysGluLeuSerGlnGluValGluArgLeuLysLeuLysLeuLys 386 426 465 LysargLeuGluargGluThrLeuGlnSerLysAspPheLysLeuGluValGluLysLeu 166 ||| :::::||||||:::||| 427 LysMetGluLeuAlaLysTyrLysLeuAlaGluLysThrGlu---ThrSerHisGluGln CAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAAGAAACTAAGAACAAGAAC 2184 GAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTG 356 CAGAAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAA TGCACCCAGCTCCATCTGAACCTGGAGAAGGAAGAACCTAACCAAAGACCTGCTGAAC 1656 TTGAATAAAACTTTAAGGTGGAGCAGGAAAAGTCATGGATGTGACGGAAAAGCTAATC ACAAAGGAGGATGAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAGGTCCTGTGAA |||||||||||||||:::||| ThrLysGluArgAspAspLeuLysAsnLysLeuLysAlaGluGluGluLysGlyAsnAsp CTGAGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGAGGTAGAAAGG |||| |LeuLeuSerArgValAsnMetLeuLysAsnArgLeuGlnSerLeuGluAlaIleGluLys 2244 CAGGCTCTCAAGGAGAAGATCCACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTC 1476 GAGCTGGAGGTGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAG 1596 1944 1536 247 1716 1776 1836 1896 407 2304 2364 147 187 227 287 307 327 367 909 8 G 8 6 8 6 8 6 8 6 8 6 8 6 8 6 상 음 상 QQ ò qq ò 8 6 8 6 8 6 8 6 8 ò

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GCTCTCAGGCCGAGTGGGAACGGCCGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGG
           ValGinThrGluAlaVal------AspAsnGluProProAspTyrLysSer
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LysMetGlnThrLysProAsnAlaAsnPheValGlnProGlyAspLeuValLeuSerHis
                                             GTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGAGAGGAGACCCCG------
                                                                                         -------GCTGTGTTCATTCGCAAATCCTTCCAGGAG---GAAAATCAC
                                                                                                                                      ATCATGAGTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTC
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| ProAsnCysGlyThrProLysGlnArgIleThrIleLeuGlnAsnAlaSerIleThrPro
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ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I) given in ABF92047 to ABF92164. A higher level of expression of (I) than normal indicates the presence of cervical cancer. Also described: (I) a vector (II) containing (I); (2) a host call (III) containing (I); and (3) assessing (MI) whether a patient is afflicted with cervical cancer, comparing the level of expression of a marker in a patient's cample, and the normal level of expression of the marker in a control non-cervical cancer sample, where a significant increase in the level of expression of the marker in the patient's sample relative to that in the control sample is an indication that the patient is afflicted with cervical cancer. (I) has cytostatic activity, and can be used in gene therapy and in vaccines. (I) is useful in detecting, characterising, therapy and the indication than cervical cancers. (I) may also be used in various prognostic assays, pharmacogenomics and in monitoring clinical trials
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                                                                                                                                                                                                                       New isolated nucleic acid molecule useful for detecting, characterizing, preventing and treating human cervical cancers, in various prognostic and diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
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14-NOV-2001; 2001US-0335936P.
                                                                                   (MILL-) MILLENNIUM PHARM INC
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Gannavarapu M, Glatt
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136   GAGATGGAGGGCAAGGATGAAGATGAGGAGGCCAGGCCCAGGGCCGGGAGGTGAAG   137   138   139	1356 CAGAAGAGGTGCTGGAGAAGCTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAA 1415	1476 GAGCTGGAGGTCCAAGAGTCCAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAG 1535	1596 GTGGATGAGGAAAAATGATGAGGAAAATAAAGGAAGGAA		1836 CTGAGCTGCAGTGTAGACTTACTAAGAAGCGCCTTGATGGCATAGAGGAGGTAGAAAGG 1895		ArgargTyralaAsnGluargaspLysAlaGlnPheLeuSerLysGluLeuGluHisVal 2123  ArgargTyrAlaAsnGluargAspLysAlaGlnPheLeuSerLysGluLeuGluHisVal 426  2124 AAACACCAAATGGCCAAGCAAAGCCATAGAGAAGGGGAGGCCTGAGCCAGGAGGC 2183  427 LysMetGluLeuAlaLysTyrLysLeuAlaGluLysTyrGluThrSerHisGluGlu 445  2184 GAACTGCGACAGGTTTCGGTGGAGGGCGTAAAAGTGTGTATTACAGGCGAGGTG 2243  446 TrpLeuPheLysArgLeuGlnGluGluGluAlaLysSerGlyHisLeuSerArgGluVal 465  2244 CAGGCTCTCAAGGAAGATCCACGAGGCTGAAAGGAAGACCAGCTGTCTCAGCTC 2303  466 AspAlaLeuLysGluLysIleHisGluTyrMetAlaThrGluAspLeuIleCysHisLeu 485
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GCAAATCCTTCCAGGAG---GAAAATCAC 2570 AAGAAACCCAIGGAACGGICCTCGGICCTC 2630
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sluAspProAsnAspGluGlySerValLeu 591 TTATGGAAGAAACTAAGAACAAGAAC 2363 ------AACGGTCCTTCCACTCCGCAG 2723 |||||| isLeuGlnAsnGly------ 622 GGCACCCCGGGGAGCTGGTCCTAGCACCA 2783 BAGCTAGAGCTTTCCAAGCGCTACAGCCGA 2423 ATGGTGGACGTGCCTGTGGCCTCCACTGGG 2483 GCGAGGAGGAGCCCCG------ 2531 SCAGCGAATGAGCTCACCATGAGGAAGTCT 2675 ::: |||{ ||| ---AspAsnGluProProAspTyrLysSer 560 --GAGTTTTTCTCTAGTACCACCGTCATT 2897 .::::::|||| .:::|||| sossible ||||||||| |luLeuGluArgTyrArgHisPheSerLys 525 CACCAGATCATGAGAACAGCACTGCCACC 2843 |||||||||||| hrProAspHisValGlnAsnThrAlaThr 662 roHisSerTyrThrSerThrAlaVallle 682 CCATTATTCCATCACCCAATGTCATGTCG 2957 CGGAAGGTGGAAGGAGCGCCTTTGCCGAC 3074 ||||| roGluSerCysGlySerLeuThrProGlu 742 ostatic; gene therapy; cancer; entral nervous system; CNS;

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and evrocated activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat disease of the peripheral nervous such as peripheral nervous injuries, peripheral nervous and contral nervous system disease, amyotropathy and localised neuropathies and central nervous system disease, amyotrophic lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, archititis and inflammation, leukaemias and c. N. S disorders. Note: The sequence data for this patent did not form bart of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                 φ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
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Zhao (
Alzheimer's, Parkinson's disease, Huntington's disease, haemostatic, amyotrophic lateral sclerosis, Shy-Drager Syndrome, chemotactic, chemokinetic, thrombolytic, drug screening, arthritis, inflammation,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-UJN-2000; 2000US-0059042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-0063460.
14-SEP-2000; 2000US-00653191.
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                                                                              Homo sapiens.
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        231 ACTATCAAAAGGCACCTCAAACCATCTGGAGAAAGTGAGAAAAAAAGACTAAGAAGTCTGTG
                                      AAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACACACTGACTAC
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                                                                                         351 CGAGAAGATGTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAGGCA
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Gaps:

US-10-788-793-1 (1-4364) x AAM41802 (1-233)

1 ArgSerCysArgGlnValGlyMetArgSerArgAsnGlnGlyGlyGluSerAlaSerAsp

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Copyright

, Xgapext , Ygapext , Fgapext , Delext

Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0,

**BLOSUM62** 

Scoring table:

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Title: Perfect :

Sequence:

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Sequence 24, Appl
Sequence 48, Appl
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Sequence 8, Appl
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Sequence 38, Appl
Sequence 32, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 4, Appl
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APPLICANT: Change, Baing
APPLICANT: Lange, Baing
APPLICANT: Cabbon, Bradford W.
APPLICANT: Globon, Bradford W.
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APPLICANT: Globon, Gary M.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER OF SCOUND NUMBER OF SEQ ID NOS: 30374
NUMBER OF SEQ ID NOS: 3077
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GENERAL INFORMATION:
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-MAXIEN-200000000.-USR-S-Dits.
-MODEL-frame+.ndf.
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1. /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2. /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
3. /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB_pep:*
4. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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                                          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                         protein search, using frame_plus_n2p model
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Listing first 45 summaries
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Query Match Length DB

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Alignment Scores: 2.63e-311 Length: 1114 Score: 5301.00 Matches: 1054 Percent Similarity: 97.13\$ Conservative: 28 Best Local Similarity: 94.61\$ Mismatches: 32 Query Match: 16.57\$ Indels: 0 DB: 16.57\$ Indels: 0	-10-788-793- 369	0 4 4	489 GGAGAAGGTCTATGAGAACCTATCAGAGGGACGGACGGAGGAGGAGGAGGAGGAGGAGGAGGA	Qy 549 GAGACGTACCGCCGCATGCTAGAGCAGCTGCTGGCTGAGAGTGTCACAGGCGCACC 608	Qy 609 GTGTACGAGGAGCGAGAAGCACACACTGACTACATGAACAAGAGCGACGAC 668	Qy       669 TTCACCAACCTGCAGAGAGAGAGAGAGTTGAAAAAGCTCCTTGAACAAGAAAAA 728	CGAGATGAG           ArgAspGlu	CACATCGAG	GAGGAGGAA           GluGluGlu	Qy 909 GAAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACGCCGGAAGCTGCTCAAGTTA 968 	Qy 969 GAAGTGGACTTCGAAGGCCTCGAGGTTTTCCCAGGAGACGAGAGAGA	Qy 1029 AATTGGGGAATCAAGAATCTGACGGGCAACTTGGACTGGTTGGCTTATCG 1088	SAAGAGCTC	1149 CAGAGCTGAGAGAAATTGCCAAAGGGGAATGTGGAAACTCCAGTTCATGGGGAA	12	13

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CGAGGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGGGGCGTACCCCCACCCGC
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TYPE: PRT
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US-10-309-851-14
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Best Local Similarity:
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Sequence 14, Application US/10309851
| Publication No. US20030108554A1. |
| Publication No. US20030108554A1. |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Saus, Juan |
| APPLICANT: Saus, Juan |
| APPLICANT: Revert-Ros, Francisco |
| TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein |
| FILE REFERENCE: 98,723-F-US |
| CURRENT APPLICATION NUMBER: US/10/309,851 |
| CURRENT FILING DATE: 2002-12-04 |
| NUMBER OF SEQ ID NOS: 38 |
| SOFTWARE: Patentin version 3.1 |
| SEQ ID NO 14 |
| CONTRACT APPLICATION NUMBER |
| SEQ ID NOS: 38 |
| SEQ ID NO 14 |
| CONTRACT APPLICATION NUMBER |
| SOFTWARE: Patentin version 3.1 |
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13	QY 1560 GACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGATGAGAGAAAAATATGATG 1619	Oy 1620 GAGAAAATAAAGCAAGAAAGAGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAG 1679	1680	1740	Qy 1800 GGTAAACTGAGGAGCGAAGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTA 1859	Qy 1860 AAGAAGCGGCTTGATGGAGGAGGTAGAAAGGBAAATAAACCGAGGTAGG 1913	Qy 1914TCGTGCAAGGGGTCTGAGTTCACCTGCCGGAAGACAATAAGATCAGAGAACTA 1967	Qy 1968 ACGCTTGAAATCGACACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGCC 2027 :::	Qy 2028 TTGATGAAGACGAATATGACCAGTTGGAGGAGAAGTTCAGAACCGAGCAGGAT 2087	Qy 2088 AAGGCAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAACACAAATGGCCAAGCACAAA 2147	OY 2148 GCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACAGGTTTCGGCTG 2207	Qy 2208 GAGGAGGCTAAAAGTCGTGATTTACAGGCGAGGTGCAGGCTCTCAAGGAGAAGATCCAC 2267	Oy 2268 GAGCTGATGAACAAGGAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAG 2327	Qy 2328 CAAAGATTATGGAAGAAACTAAGAACAAGAACATGGGGAGGGA	OY 2388 ACCAAGGAGCTATCCAAGGCTACAGCCGAGGCTCTCAGGCCAGTGGGAACGC 2447	Qy 2448 CGAAGGATGGTGGCTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGG 2507	Qy 2508 GATGCTGCGGAGGAGGACCCCG	Qy 2538 TTCATTCGCAAATCCTTCCAGGAGGAAAATCACATCATGAGTAATCTTCGACAGGTA 2594 ::::::             Db 823 IleAsnGlyGlnLeuTyrGluGluSerGluAsnGlnAsp	GGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGTAT 26
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 1133
TYPE: PRT
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2444.50
64.31%
46.08%
31.62%
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US-10-309-851-16
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APPLICANT: Revert-Ros, Francisco
TITLE OF INVENTION: GIPS, a Family of Polypeptides with Transcription Factor Activity
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFERENCE: 98,723-F-US
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|HisLeuGlySerProTyrMetGlnAla------ValAlaSerProValArgProAla 1081
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LeuAlaValThrGlySerAlaSerSerProGluGlnGlyArgSerProGluProThrGlu
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                                                                       CCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAGA
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Publication No. US20030108554A1
GENERAL INFORMATION:
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609 GlnAspSerGlyLysSerThrThrAlaLeuHisGlnGluAsnAsnLysIleLysGluLeu	1968 629	2028	OY 2088 AAGGCAAACTTCCTCTCCCAGCAGCAGGAAATCAAACACCAAATGGCCAAGCACAAA 2147	Qy 2148 GCCATAGAGAGAGGCGTGAGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTG 2207	Qy 2208 GAGGAGGTAAAAGTCGTGATTTACAGGCCGAGGCTGCAGGCTCTCAAGGAGAAGATCCAC 2267	Qy 2268 GAGCTGATGAACAAGGAGGCGGCTGTCTCAGGTCGAGTCGATTCGGTCCTTCAG 2327	Qy 2328 CAAAGATTTATGGAAGAAACTAAGAACAAGAACATGGGGAGGGA	Qy 2388 ACCAAGGAGCTAGAGCGCTACAAGCGCTACAGCGAGCGCCGAGTGGGAACGGC 2447	Qy 2448 CGAAGGATGGTGGCCTGTGGCCTCCACTGGGGTGCACCGACCG	Qy 2508 GATGCTGCGGAGAGAGCCCCG	QY 2538 TTCATTCGAAATCCTTCCAGGAGGAAAATCACATGAGTAATCTTCGACAGGTA 2594 1::::::::             Db 823 IleAsnGlyGlnLeuTyxGluGluSerGluAsnGlnAsp835	Qy 2595 GGCCTGAAGAAACCCATGGAACGGTCCTCGGTCCTCGACAGGTAT 2639 :::	Qy 2640 CCCCCAGCAGCGAATGAGCTCACCATGAGGAAGTCTTTGGATTGATAGAAAAGA 2699	OY 2700 GAAAACGGTCCTTCCACTCCGCAGAGAAAAGGCCCAGGCCAAACCAG 2747	Qy 2748 GGTGCAGGGCACCCCGGGGAGCTGGTCCTAGCACAAGCAGGGCCAGCCCTACACATC 2807	Qy 2808 CGTGTGACACCAGATCATGAGAACAGCACTGCCACCTGGAGATCACAAGCCCCCACATCT 2867 :::	OY 2868 GAAGAGTTTTCTCTAGTACCACCGTCATTCCTTAGGCAACCAGAAACCA 2921	OY 2922 AGAATAACCATTATTCCATCACCAATGTCATGTCGAAAAGCCCAAAAGTGCAGAT 2978  OH
249 LeuThralaGlnLeuThrLeuGlnArgGlnLysIleGlnGluLeuThrThrasnAlaLys 268	900 GAGGAGGAAGAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTG 959	960 CTCAAGTTAGAAGTGGACTTCGAAGGCCTCGAGGTTTTCCCAGGAGGAGGG 1019	1020 ATGAACGCCAAATTGGCGAATCACAAGAACCTGCAACTTCGACTCAAACTGGTT 1079		CTCCAGTCTC	1200 ATGCGGAAGTGGAGAGCGCAAGCGCGTGCTTGAGATGGAGGGCAAGGATGAAGAG 1259	GGAAGAACAC      qGluThrLeu				CCTCAAAGAT	GACCTTACAAAGCTGAAGTCCTTGACTGATGGAGGAAAAATGATGATGATGATGATGATGATGATG		1680 CAGGGAAAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGATTTTAAAA 1739 		GGTAAACTGAGGAGGAGAAGAAGGGCCCTGTGAACTGAGCTGCAGTGTAGACTTACTA        ::::::		

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                                   LeuThrAlaGlnLeuThrLeuGlnArgGlnLygIleGlnGluLeuThrThrAsnAlaLys
                                                                                                       900 GAGGAGGAAGAAAAACTCAAAGCGGTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTG
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                                                                                                                                                                                                                                                                                                                     GCCAATCGGAAGGAGGAG---GATGTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAA 251
                                                                                                                                                                                                                                                                                         HisThr------ysGlyHisSerPheGlnGlyProLysAsnMet 31
Publication No. US20030108554A1
GENERAL INFORMATION
APPLICANT: Saus, Juan
APPLICANT: Revert-Ros, Francisco
TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Fr
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
FILE REFRENCE: 98,723-F-US
CURRENT APPLICATION NUMBER: US/10/309,851
CURRENT APPLICATION DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10.0
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|SerAspGluPheIleCysLeuLeuGluGluGysGluArgLeuLysLysLeuIleAsp
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Matches:
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Indels:
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69.55%
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                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-851-10
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    SerAsnSerAsnSerSerVallleThrThrGluAspAsnLysIleHisIleHisLeu
                                           GGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGCGTGAGCCCCAGTTATCACC
                                                                                                                                                      SerAlaProLeuGlnAspAsnArgThrGlnGlyLeuIleAsnGlyAlaLeuAsnLysThr
                                                                                758 GlySerProTyrMetGlnAla-----ValAlaSerProValArgProAlaSerPro
                                                                                                                        3345 GTCCGGCCTGTCAACGTGACAGCGGAGAAGGAGGTTTCTACAGGCACAGTCCTTCGCTCT
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|ThrProThrAlaThrProLeuProArgGlnSerGln 816
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CRGANISM: Homo sapiens
US-10-309-851-24
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                                                         ATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGA 2333
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GluAspProAsnAspGluGlySerValLeuSerPheLysCysSerGlnSerThrProCys 546
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---AspAsnGluProProAspTyrLysSerLeuIleProLeuGluArgAlaValIleAsn 515
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698 ValThrGlySerAlaSerSerProGluGlnGlyArgSerProGluProThrGluIleSer 717
                                                                                     481 IleSerAspProGlnValPheSerLysGluValGlnThrGluAlaVal------
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GINPHELEUSETLYSGIULEUGIUHisvalLysMetGlübeuAlaLysTyrLysLeuAla GAGAAAGGGGGCCCTCAGCAGCAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGGG GAGAAAGGGGGCCCTCAGCAGCTGAACTGCGACACAGGTTTCGGCTGGAGGGG GIULYSThrGluThrSerHisGlüGlüTrpLeuPheLysArgLeuGlüGlüGlüGlüGlüGlüTrpLeuPheLysArgLeuGlüGlüGlüGlüGlüGlüGlüGlüGlüGlüGlüGlüGlüG
ATGGTGGACGTGCTGTGG

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----GACAGGTATCCCCCA 2645
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                                                                                                                                          GCAGCGAATGAGCTCACCATGAGGAAGTCTTGGATTCCTTGGATGAGAAAAAGAGAA--- 2702
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                                                                             ::: ||| ::: ||| GludlySerValLeuSerPheLysCysSerGlnSerThrProCys 505
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|HisLeuGlnAsnGly------LysMetGlnThrLysProAsnAlaAsnPhe
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764 ThrProThrAlaThrProLeuProArgGlnSerGln 775
175 GlyGlnLeuTyrGluGluSerGluAsnGlnAsp----
                                               AAGAAACCCATGGAACGGTCCTCGGTCCTC----
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367 GluAsnAsnLys1leLysGluLeuSerGlnGluValGluArgLeuLysLeuLysLeuLys 386
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APPLICANT: Zhao, Xumei
APPLICANT: Montahan, John
APPLICANT: Montahan, John
APPLICANT: Gamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Ganavarapu, Manjula
APPLICANT: Hoersh, Sobsetian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILLE REPRENCE: NIL-035
CURRENT APPLICATION NUMBER: US 60/298,159
PRIOR FILLING DATE: 2001-06-13
PRIOR FILLING DATE: 2001-06-13
PRIOR FILLING DATE: 2001-06-13
PRIOR PAPLICATION NUMBER: US 60/298,155
PRIOR PAPLICATION NUMBER: US 60/335,936
PRIOR PAPLICATION NUMBER: US 60/335,936
PRIOR SEQ ID NOS: 238
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 48
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LysArgLeuGluArgGluThrLeuGlnSerLysAspPheLysLeuGluValGluLysLeu 166
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| MetValValAspGluGlnGlnArgLeuThrAlaGlnLeuThrLeuGlnArgGlnLysIle 20
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|GlnGluLeuThrThrAsnAlaLysGluThrHisThrLysLeuAlaLeuAlaGluAlaArg 40
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Matches:
Conservative:
Mismatches:
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1645.50
64.16%
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; LENGTH: 752
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-48
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Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE COCATION: (416)
LOCATION: (416)
9-925-302-495
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159 IleProLeuGluArgAlaValIleAsnGlyGlnLeuTyrGluGluSerGluAsp 178
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| 190 PheLysCysSerGlnSerThrProCysProValAsn------ArgLysLeuTrp
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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780.50
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Local Similarity:
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                                   2901 ACCTTAGGCAACCAGAAACCAAGAATAACCATTATTCCATCACCCAATGTCATGTCGCAA 2960
                                                                               2961 AAGCCCAAA---AGTGCAGATCCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACG 3017
                                                                                                                           3018 ATTACTACTATTCCAGAGAGAAGAGCCCGGAAGGTGGAAGGAGGGCCTTTGCCGACAGG 3077
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::: ||| :::||| :::|||| 321 MetalaThrPheAlaArgAlaGInThrProGluSerCysGlySerLeuThrProGluArg 340
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381 ArgGlnSerSerTrpGlnPheGlnArgSerAsnSerAsnSerSerVallleThrThr 400
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acide, Proteins and Antibodies
FILE REFERENCE: PAIGN UNDEER: US/09/925,302
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR PRIOR DATE: 2000-03-08
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 895
SOFTWARE: Patentin Ver. 2.0
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Matches:
Conservative:
Mismatches:
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FEATURE:
NAME/KEY: SITE
LOCATION: (8)
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Best Local Similarity:
Query Match:
DB:
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US-10-788-793-1 (1-4364) x US-09-925-302-495 (1-439)

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2067 AAGTICAGAACCGAGCAGGAIAAGGCAAACTICCTCTCCCAGCAGCTCGAGGAAATCAAA 2126
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206 IleProTrpMetLysSerLysGluGlyHisLeuGlnAsnGly------Lys 220
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                                                                                                                                                                                                                                                                                                               241 ProGlyGlnProLeuHisIleLysValThrProAspHisValGlnAsnThrAlaThrLeu
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Sequence 6, Application US/10309851

Publication No. US20030108554A1

GENERAL INFORMATION:

APPLICANT: Saus, Usan

APPLICANT: Revert-Ros, Francisco

TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity

TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein

TITLE REFERENCE: 98,723-F-US

CURRENT APPLICATION NUMBER: US/10/309,851

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 265
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                                                                     PhevalThrProLysLysValLeuGluAlaLeuGlnArgAspAlaPheGlnAlaLysSer 128
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|GlnGluIleLysSerGlnGluGluLysGluGlnGluLysGluLysArgValThrThrLeu
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ORGANISM: Homo sapiens
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Fublication No. US20030108554A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saus, Usan
TITLE OF INVENTION:
TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
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                                                                                                                                                                            3198 AAACAAACTGTTCCAGCCCCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACCACG 3257
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                           341 ThrMetSerProlleGlnValLeuAlaValThrGlySerAlaSerSerProGluGlnGly 360
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381 ArgGlnSerSerTrpGlnPheGlnArgSerAenSerAenSerSerVallleThrThr 400
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ORGANISM: Homo sapiens
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951 CAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACAAAGGCCTCGAGGTTTTCCCAAGGAG 1010
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181 AsnAlaLysGluThrHisThrLysLeuAlaLeuAlaGluAlaArgValGlnGluGluGluGl
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                                                                                                                 351 CGAGAAGATGTCATCCACATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTGGAGGCA 410
                                                                                                                                                                                                                                                        711 CTCCTTGAACAAGAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAACGCTAAAGCGGCTC 770
                                                                                                                                                                                                                                                                                                                                                                                                                                               771 AACAAACTTGGAGATGAGCTTGTGAAGCTCAAGTCCTTCGCCCTCATGTTGGTGGACGAG 830
                                                                                                                                                              111 CACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATCCTT 470
                                                                                                                                                                                                            471 GCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTGGACAGA 530
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41 AlaLysSerThrProTrpGlnGluAspIleTyrGluLysProMetAsnGluLeuAspLys 60
                                                                                                                                                                           651 ATGAACAAGAGCGACGACTTCACCAACCTGCAGGAGCAGGAGCGAGAGGTTGAAAAAG
         Length:
Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20030108554A1
GENERAL INFORMATION:
APPLICANT: Saus, Juan
APPLICANT: Revert-Ros, Francisco
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TITLE OF INVENTION: GIPs, a Family of Polypeptides with Transcription Factor Activity TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein FILE REFERENCE: 98,723-F-US CURRENT APPLICATION NUMBER: US/10/309,851 CURRENT APPLICATION DATE: 2002-12-04 NUMBER OF SEQ ID NOS: 38 SOFTWARE: PatentIn version 3.1 SEQ ID NO 38 LEGITION OF 38 SOFTWARE: PatentIn Version 3.1 SEQ ID NO 38 LEGITION OF 38 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 284 SOFTWARE: 285 SOFTWARE: 284 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOFTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SOTTWARE: 285 SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2460 GACGTGCCTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGGGATGCTGCGGAG 2519
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	293 ATTCCANCACCAATGTCATGTCGCAAAAGCCAAAAGTGCAAATCATCTCGGC 2990  291 CAGAACGAGCATGTCATGTCGCAAAAGCCAAAAGTGCAAACCAACTCTCGGC 2990  292 CAGAACGAGCATGTCATGTCGCAATACTATTTCAAGAGAAAAGACCCGAA 3050  293 CCAGAACGAGCATGTCCCTGTCACTATTTTTCAAGAGAAAAAAAA
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Db 220 LeuGluGlnGlyMetSerProlleThrMetAlaThrPheAlaArgAlaGlnThrProGlu 239  Oy 3051 GGTGGAAGGGCCTTTGCCGACAGGCCTGCACCCAAATCATGACGGTGTC 3110  240 SerCysGlySerLeuThrProGluArgThrMetSerProlleGlnValLeualaValThr 259  Oy 3111 ACATCTGCAGCTCCCACAAATCGCTGTCTCTCCTGAATCTCAGGAAGTGCTATGGA 3170  Db 260 GlySerAlaSerSerProGluGluGlyArgSerProGluProThrGluIleSerAlaLys 279  Oy 3171 AGGACTATCCTCAAAGTCACCGGAAAAAAAAAATTCACATTCACGGAAGTAC 3230  Db 280 HisAlaIlePheArgValSerProAspArgGluSerSerTrpGlnPheGlnArgSerAsn 299  Oy 3121 AACTCCAATGTCACACCGGGAAGAAAAAAAATTCACATTCACCTGGGTTCT 3290  320 CHISALAIIlePheArgValSerProAspArgGluSerSerTrpGlnPheGlnArgSerAsn 299  Oy 3291 CAGTTTAAGCGATCTCTGGGCCTGAGGGGAGTATCACCTGGGTTCT 336  Oy 320 CAGTTAAGCGATCTCTGGGCCTGAGGGGAGTAATCACCTCCGGG 3350  Db 320 ProTyTMetGlnAla	NEBULT 15   Sequence 22, Application US/1030951

367 ThrAlaThrProLeuProArgGlnSerGln 376

Search completed: September 7, 2004, 15:14:10 Job time: 547.5 secs

148, App 148, App 1, Appli 2, Appli 4, Appli

29, Appl 2, Appli 2, Appli 2, Appli 2, Appli

Perfect score:

Sequence:

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Sequence 296, App
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Patent No. 6544766

GENERAL INNORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Variaberg, Eugeni
APPLICANT: Variaberg, Eugeni
APPLICANT: Variaberg, Eugeni
APPLICANT: Variaberg, Eugeni
APPLICANT: Variaberg, Eugeni
APPLICANT: Yu, Ming
TITLE OF INVENTION: Human kinesins and methode of producing
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: Cytopo36
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 31
LENGTH: 2662
            US-08-467-781-4

US-08-487-4

US-08-487-4

US-09-452-294-1

US-09-452-294-1

US-09-153-06160-4

US-09-153-06160-4

US-09-1572-19-2

US-09-572-19-2

US-09-976-594-296

US-09-976-594-296

US-09-866-108A-15753

US-08-685-576-4

US-08-685-576-1

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US-08-685-576-1

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US-09-168-595-148

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US-09-976-594-726

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US-08-533-306A-4
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Matches:
Conservative:
Mismatches:
Indels:
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473.50
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20.61%
6.12%
 Percent Similarity:
Best Local Similarity:
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ORGANISM: Human
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Query Match:
 Command line parameters:

"MODEL=frame+ n2b model - DEV=xlp
-0=/cgn2_1/USFTO_spool_p/US10788733/runat_07092004_134022_10839/app_query.fasta_1.4551
-0=/cgn2_1/USFTO_spool_p/US10788733/runat_07092004_134022_10839/app_query.fasta_1.4551
-DB=I8Bued_Patente_AA - OFWT=fastan - SUFFTX=rai - MINMATCH=0.1 - LOOPCT=0
-LOOPEXT=0 - UNITS=bits - START=1 - RMD=1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15
-MODE=LOCAL - OUTFWT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXEN=200000000
-USRE-US10788793_GCN 1 117 @runat_07092004 134022 10839 - NCFU=6 - ICPU=3
-NO MMAP. -LARGEQUERY - NEG_SCORES=0 - WAIT - DSPELOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPPO=10 - XGAPPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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                                                                                                                                                                        Sequence 31,
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/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                       - protein search, using frame_plus_n2p model
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US-08-328-254-6
US-08-353-700-1
VS-08-353-700-1
US-08-056-200-94
US-08-800-644-94
US-09-914-259-11
US-09-310-187A-1
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Maximum Match 100%
Listing first 45 summaries
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đ	1421 GluMetLeuGlyLeuSerLysArgLeuGlnGluSerHisAspGluMetLysSerValAla 1440	à	1218 CTGCGCAAGCGC
ò	294 TIAICCAAGGAGCACCTCAICCAGCTCCTGAGTATCAIGGAAGGGGAGTIGCAGGCT 350	\$ £	
qq	1441 LysGluLysAspAspLeuGlnArgLeuGlnGluValLeuGlnSerGluSerAspGlnLeu 1460	3 8	2012 redargery rec
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ò	408 GCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGAGATGCCATC 467	Š	1326 AAGGAACTIAG
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셤	:::	qq	1884 LysServalMet
ò	CGCACCGTGTACGAGAAACGAGAAAGCACAAAACAACACACTGACTAC	ò	1542 GAGTTAAGCCTC
7 A		qq	1904 ArgAspGlnLev
6	ATGAACAAGAAGAAGAACAACTAACCTAGCTAGAAGAAGAAGAAAGA	λŏ	1602 GAGAGGAAAAT
i d		qa	1924 GluLeuLysThr
Š	CTCTTGAACAAGAAAAAGCTTTACCAAGCCGGAAAAGAAAAAGCAAAACCGAAAAAAAA	δδ	1662 AAAAACTTTAAG
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. A	GlulleValAlaLysMetLysGluSerGlnGluLysGluTyrGlnPheLeuLysMetThr	qa	1957 GlnLysAspLeu
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1733 Gln	
1110 GAG	GAGACCAATAAAAGCCTTCAGAAGGCAGAGGAAGAGCTCCAGGAGCTG 1157
1158 AGA( ::: 1772 Gln(	AGAGAGAAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAGTGT 1217 :::   :::::  GInGluGluLeuArgIleAlaHisMetHisLeuLysGluGlnGlnGluThrIleAspLys 1791
1218 CTGCG        1792 LeuAr	CTGCGCAAGCGCGTGCTTGAGATGGAGGCAAGGATGAAGAGATCACG 1265        
1266 AAG	AAGACCGAGGCCCAGTGCCGGAGCTGAAGAAGAGCTCCAAGAGGAAGAACACCACAGC 1325 :::                 AsnSerAsnAlaLysLeuGlnGluLysleGlnGluLeuLysAlaAsnGluHisGlnLeu 1831
1326 AAGG 1832 Ile	AAGGAACTTAGACTAGAAGGGGGGAGAGGGGGAGGATGTCTGAGCTGGAGAAGCTG 1385    ::::::    :::    :::
1386 1852 Lysi	GAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCCAGCTCCAT 1430
1431 CTG	CTGAACCTGGAGAAGGAGAAGACCTAACCAAAGACCTGCTGAACGAGGTGGTC 1490
1491 AAG? 	AAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCC 1541        :::        LysSerValMetLysGluArgAspAsnLeuArgArgValGluGluThrLeuLysLeuGlu 1903
1542 GAG7 1904 Arg <sup>2</sup>	GAGTTAAGCCTCAAAGATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGAT 1601        :::     :::     :::     ::: ArgAspGlnLeuLysGluSerLeuGlnGluThrLysAlaArgAspLeuGluIleGlnGln 1923
1602 GAG     1924 GluI	GACAGGAAAATATGATGGACAAAATAAAGCAACAAGAAGAGAAAGTGGATGGA
1662 AAAA ::: 1944 Glu-	AAAAACTTTAAGGTGGAGCAGGGAAAAGTCATGGATGTGACGGAAAAGGTAATCGAGGA 1721 :::
1722	AGCAAGAAGCTTTTAAAACTCAAATCTGAAATGGAGAAAAGGAGTACAGTCTGACAAAG 1781 
1782 GAGA ::: 1977 LysG	GAGAGGGATGAGCTGATGGGTAAACTGAGGAGGAGGAAGAAGGTCCTGTGAACTGAGC 1841 :::
1842 TGCA 1988	TGCAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGGGGGGG
1902 AACC 2006 GluE	AACCGAGGTAGGTGGGAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGA 1961 
1962 GAAC  :::   2019 GlnI	GAACTAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAG 2021 :::
2022 GGGG 2035	GGGGACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACCGAG 2081 
2082 CAGG	CAGGATAAGGCAAACTTCCTCCTCCAGCAGCTCGAGAAATCAAA 2126 :::   :::

-	PhelleAlaThrLeuArgGluMetIleAlaArgAspArgGlnAsn 20	AMATGGCCAAGCACAAGACATIA	Qy 3030	::: :::     ::: 3380     :::      :::     :::      :::      :::      :::      :::      :::      :::      :::      :::       :::      :::      :::      :::      :::       :::       :::      :::	GGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAG2246	nArgLeuSerLeuAspLeuGluLysGluIleGluPheHisArg 2129	Y 3.50 ILICAGGARAGAGGAGAAGATCCAC 2267 Db 2415 IvsGludlufledluAsplentvsMetivs	sTyrValLeuSerTyrValThrLysIleLysGluGluGlnHis 2149	GAAGACCAGCTGTCTCAGGTCGAGTTTCGGTCCTTCAG 2327  11: Db 2435	Oy 3267 AAAATTCACATGGTG 2156	AGAAACTAAGAACATGGGGAAGGAAGGTCCTCAATCTG 2387  AGAAACTAAGAACATGGGGAAGGAAGGTCCTCAATCTG 2387  Db 2454	uvaigiutyboinnyboinneureurietybilegilmibudu TTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAAACGGC		GCCTGTGGCCTCCACTGGGGGCGGTGCTGCGGG 2507	2494	SACCCCGCCTGTGTT		2534 Db 2534		PheAspleGluLvsLeuLvsAsnGlvYileGluAsnAspArglleCvsGlnValThrCys	Qy 3450	2574 GlyThrAlaS	-CTCACCATGAGAAGTCTTGGATTCCTTGGATGAGAAAAAGGGTCCT 2711	2293 <u>2331</u> . Qy 3531	AGGGCCCAGGCCAAACCAGGGTGCAGGGCACCCCGGGGAGCTG 2771 Db 2613	8AsnGluLys	283	ACATICHGAAGAGHHHHHCHCHAGGAACCACC 2891	2326 4	AAACCAAGAATAATCCATTATTCCATCACCCAATGTC 2951 US-08-875-435B-3		2952 ATGTCGCAAAAGGCCCAAAAAGTGCTACTCTCGGCCCAGAACGACCATG 3005 ; GENEKAL INFORMATION: APPLICANT: Haseawa, Kazuhide ; APPLICANT: Arakawa, Emi
	2052 ArgAspGln	UY 2127 CACCAAATGGCCAAGCACAAAGCC       ::  Db 2070 HisGlnValLysProGluLysArg	2154GAGAAA	2090 LeuArgGluLysCysSerArgIl	Qy 2196 AGGTTTCGGCTGGAGGAGGCTAAA.	Db 2110 HisTyrGluCysLeuAsnArgLeu	Qy 2247	<pre>Db 2130 IleMetLysLysLysLeuLysTyrVal</pre>	2268	2150	Qy 2328 CAAAGATTTATGGAAGAAGAACT.	2388 ACCAAGGAGCTAGAGCT	::::: :::::: 2177 GlnGlnAspCysAspVa	Oy 2448 CGAAGGATGGTGGACGTGCCTGTG	:::   ::: ::: Db 2196MetAspLeuHisIle	Qy 2508 GATGCTGCGGAGGAGAGACCCCG	Db 2206 AspPheSerGluSerGluPhePro		7777	2221 PheAspileGluLysLeuLysAsn	2631	bb 2261 AsnAsnPhePheAsnAsnArgIle	Qy 2658CTCACCATGAGGAAGTCT"	2281	2712	2294	Qy 27/2 GICCIAGCACCAAAGCAGGGCCAG			Qy 2892 GTCATTCCTACCTTAGGCAACCAG	Db 2327AsnLys	OY 2952 ATGTCGCAAAAGCCCAAAAGTGCA

nLysGluLeuGluValThrAsnAspIleIle 2379 GAGCGCCTTTGCCGACAGGCCTGCATCCCCC 3089 AGCTCCCACTGAAATCGCTGTCTCCTGAA 3149 -----GGTŢĊŢĊĄĠTTTAAGCGATCTCCT 3308 nLeuArgArgSerGlnGlnAlaGlnAspThr 2473 TATCACCGTCCGGCCTGTC----- 3356 .:: ::||||:::
.nProSerAsnLysProLeuThrCysGlyGly 2493 ------3368 ::::::
aLeulleLeuLysSerGluHisIleArgLeu 2513 ------3395 nAsnGluGlnLeuIleLysGlnLysAsnGlu 2533 AAGA---- 3428 : inGluValLysThrTrpLysGluArgThrLeu 2553 ------CCCGGTGCTAGCAAAGTGACC 3449 ||| ::: ||||||||| 8GluAsnSerProlysSerProlysValThr 2573 CCCGGTCACAA----- 3483 AGTGT---CAGGACAAGATGGGTCATCTCAG 3530 -----CCTGTCACGATTACTATT 3029 ::: rAsnLysCysLeuGluLysThrLysGluThr 2399 erCysPhePheAspSerArgSerLys-SerL 2613 AspAsnSerSerLeuGlyLeuCysProGluV 2633 AAAAGGTATGAA----- 3571

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                 991
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| 1085 LeuAlaLysLysGluGluGluLeuGlnAlaAlaLeuAlaArgLeuAspGluGluIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LeuValMetAsp
                                                                 954 AAGCIGCICAAGIIAGAAGIGGACIICGAACACAAGGCCICGAGGIITITCCCAGGAGCAC
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1052 GluLeuGluLysLeuLysArgLysLeuGluGlyAspAlaSerAspPheHisGluGlnIle
                                                                                                                                                                                                                                                                                                           1074 CTG-------GTTGGCTTATCGCAAAGGATTGAGCAAGGAA
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APPLICANT: Mateuda, Yuzuru
APPLICANT: Takahashi, Kateuhito
APPLICANT: Takahashi, Kateuhito
APPLICANT: Sugahara, Michihito
APPLICANT: Sugahara, Michihito
APPLICANT: Sugahara, Michihito
TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
TITLE OF INVENTION: VECTOR DNA, MICROORGANSIM CARRYING THE RECOMBINANT DNA, AND
TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: RECOMBINANT DNA
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TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: NUMBER: US/08/875,435B
CURRENT FILING DATE: 1997-07-25
FRIOR APPLICATION NUMBER: PCT/JP96/00134
RROR PILING DATE: 1996-01-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: SEGSEE FOR Windows Version 4.0
SEQ ID NO 3
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Matches:
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TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
TITLE OF INVENTION: FOR MYCSIN HEAVY CHAIN SM1 ISOFORM PROTEIN INSERTED INTO
TITLE OF INVENTION: VECTOR DNA, MICROCREANSIM CARRYING THE RECOMBINANT DNA, AND
TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: RECOMBINANT DNA
TITLE OF INVENTION: RECOMBINANT DNA
CURRENT APPLICATION NUMBER: US/08/875,435B
CURRENT FILING DATE: 1997-07-25
PRIOR PILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FABLEEQ for Windows Version 4.0
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Best Local Similarity:
Query Match:
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Oda, Shoji Matsuda, Yuzuru Takahashi, Katsuhito Sugahara, Michihiro

APPLICANT: Hasegawa, Kazuhide APPLICANT: Arakawa, Emi APPLICANT: Oda, Shoji APPLICANT: Matsuda, Yuzuru APPLICANT: Takahashi, Katsuhito APPLICANT: Sugahara, Michihiro

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| CysAspIleSerLysGluHisThrSerGluThrThrGluArgThrProLysHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IleSerGluLeuSerPheSerGlyProAsnAlaLeuValProMetAspPheLeuGly 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||
|IeuLeuHisVallleGluAspArgAspArgLysValGluSerLeuLeuAsnGluMet 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluLeuAspSerLysLeuHisLeuGlnGluValGlnLeuMetThrLysIleGluAla 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::: ||||||| :::|||||||
|IleGluLeuGluLysIleValGlyGlu-----LeuLysLysGluAsnSerAspLeu 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :::::: ||||
LysSerSerArgGluAspIleGlyAspAsnValAlaLysValAsnAspSerTrpLys 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||
|GluLysLeuGluTyrPheSerCysAspHisGlnGluLeuLeuGlnArgValGluThr 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TCTAACGGGCATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTAAGGGCCCCTCAGAAGATGCAAAAAAAAAAGAACAAGGCCAATCGGAAGGAGGAGGAT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGGGAGTTGCAG----GCT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGATGTCATCCAC----ATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGA--- 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTGCTCAAGAGAAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACT 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGTCGACAACAGGTGGGAATGAGATCACGAAAT-----CAAGGTGGAGAAAGT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACTGGAGGAAAAGCAGAAGGAGACGTACCGCCGCATGCTAGAGCAGCTGCTGCTG 584
                                                                                                                                                                                                                                                                                                  2482
306
245
521
476
                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-4364) x US-08-328-254-6 (1-2482)
IE/DOCKET NUMBER: P-CJ 1191
IICATION INFORMATION:
RE: (619) 535-9001
(619) 535-8949
FOR SEQ ID NO: 6:
HARACTERISTICS:
2482 amino acids
mino acid
mino acid
:: linear
:: linear
YPE: protein
                                                                                                                                                                                                                                                                                                    6.14e-22
440.00
35.59%
19.77%
5.69%
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us-10-788-793-1.rai

ą.		QQ	2672 AsnAlaSerLeuGlnAspThrLeuGluValLeuGln5
i	1177177	ò	2130CAAATGGCCAAGCACAAGCC
डे ह	1425 CICCAICIGANCCIGGAGANAGANACCIAACCAAAGACCIGCIGAACGAGCIG 1481	ΩD	:::        ::: 2692 GluLeuGluLeuThrLysMetAspLysMetSerPheV
3 8	Araciulicecinicientistedy boruceluserry binrala valorumet Leuceluabildine d	ζō	2172 AGCCAGGAAGCCGAACTGCGACACAGGTTTCGGCTGC
5		q	:::::    2712 AlaLysGluThrGluLeuGlnArgGluMetHisGluM
3 8	הלפקיתים משנים ישנים אינותים מ	ò	2232 CAGGCCGAGGTGCAGGCTCTCAAGGAGAAG
Š i		q	::: 
සි	2381 ThrGluGlnSerLeuAspProProIleGluGluGluHisGlnLeuArgAsnSerIleGlu 2400	ò	2268 GAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCC
ò	1569 AAGCTGAAGTCCTTCACTGTGATGCTGGATGAGGAAAAATATGATGGAG 1622	. q	2752 GluileLvaSerSerIvaAspGlnLeuLvsGluLeu1
අු	2401 LysLeuArgAlaArgLeuGluAlaAspóluLysLysGlnLeuCysValLeuGln 2418	}	
ò	1623 AAAATAAAGCAAGAAAGAGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAGCAG 1682	3	:::
셤	2419 GlnLeuLysGluSerGluHisHisAlaAspLeuLeuLys 2431	a 8	
ò	1683 GGAAAAGTCATGGATGTGACGGAAAAGCTA	Š 7	2378 GICCICAAICIGACCAAGGAGCIAGAGCIIICCAAGG
අු	2432 GlyargValGluAsnLeuGluArgGluLeuGluIleAlaArgThrAsnGlnGluHisAla 2451	an o	
ò	1713ATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAA 1751	डे :	2436 AGTGGGAACGGCCGAAGGATGGTGGACGTGCTGTGC
QQ	2452 AlaLeuGluAlaGluAenSerLy8GlyGluValGluThrLeuLy8AlaLy81leGluGly 2471	a a	
'n	1752ATGGAGGAAAAAGAAGTACAGTCTGACAAAGGAGAGAGAT 1790	ð	
qq	2472 MetThrGlnSerLeuArgGlyLeuGluLeuAspValValThrIleArgSerGluLysGlu 2491	д С	GluGluCysLeuS
ò	1791 GAGCTGATGGGTAAACTGAGGAGGAGGAAGAAAGGTCCTGTGAACTG 1838	ò	2556 CAGGAGGAAAATCACATC
q	2492 AsnLeuThrAsnGluLeuGlnLysGluGlnGluArgIleSerGluLeuGluIleIleAsn 2511	đ	2849 LysGluGluLeuAsnAsnSerLeuLysAlaThrThrG
ò	1838 1838	δ	2574ATGAGTAATCTTCGACAGGTAGGCCTGA
q	2512 SerSerPheGluAsnIleLeuGlnGluLysGluGlnGluLysValGlnMetLysGluLys 2531	අු	2869 ThrLysMetAspAsnLeuLysTyrValAsnGlnLeul
ò	1839AGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGATGGCATAGAGGAGGTAGAA 1892	ò	2622 TCGGTCCTCGACAGGTATCCCCCAGCAGCGAATGAGC
q		අු	2889 GlyLysMetLysLeuLeulleLysSerCysLysGlni
à		ò	2682 CCTTGGATGAGAAAAGAGAAAACGGTCCTTCCACTC
q	:::  abysGluGlnAsnLeuSerSerGlnVal	qq	2907IleLeuGlnLysGluLeuSerGlnLeuGlnAlaA
ò		ò	2742 AACCAGGGTGCAGGGCACCCCGGGGAGCTGGTCCTAC
q	 2572 GluCysLeuGluLeuGluLysAlaGlnLeuLeuGlnGlyLeuAspGluAlaLysAsnAsn 2591	q	2922
ò	GACAAT	ò	2802 CACATCCGTGTGACACCAGATCATGAGA
셤	2592 TyrileValLeuGlnSerSerValLysGlyLeulleGlnGluValGluAspGlyLysGln 2611	qq	2929 AspThrLysValAspGluLeuThrThrGluIleLysG
è	AAGATCAGAGAACTAAACGCTTGAAAATCGAGAACTGAAAGAAA	ò	2853 ACAAGCCCCACATCTGAAGAGTTTTTCTCTAGT
; 음	2612 LysLeuGluLysLysAspGluGluIleSerArcLeuLysAspGlnAspGluGlu 2631	අධ	2949 LysThrLysGluAlaAspGluTyrLeuAspLysTyrC
ò		ò	2886ACCACGTCA
: 음	.euTroLveGluGlnAsn	<b>원</b>	2969 LysLeuGluLysAlaLysGluMetLeuGluThrGlnV
ò		ò	2919 CCAAGAATAACCATTATTCCATCACCCAATGTCATGT
: 셤	LeuGluLeuArgAsnLeuThrValGluLeuGluGlnCyslleGlnValLeuGlnSerLys	q	2989
ò	GAGGAAATCAAACAC	ò	2979 CCTACTCTCGGCCCAGAACGAGCCATGTCCCCTG
	· · · · · · · · · · · · · · · · · · ·	qq	2997 ProLeuLeuGlyProValValProGlyProSerProI

::: ::: ||||||| ----IleAspLeuLeuLysSerSer 2848 GAAGAAACCCATGGAACGCTCC--- 2621 |||||||| uLysLysGluAsnGluArgAlaGln 2888 GGAGGAGCTAAAAGTCGTGATTTA 2231 |||::: :::||| uMetAlaGlnLy8ThrAlaGluLeu 2731 :::
aGlyGluLeuGlnLeuLeuLeuGlu 2751 CCAAGTCGACTATTCGGTCCTTCAG 2327 | :::::: ||| ||||::: uThrLeuGluAsnSerGluLeuLys 2771 TAAGAACAAGAACATGGGGAGGAG 2375 GCGCTACAGCCGAGCTCTCAGGCCG 2435 :::: LygLygHigGlnAlaLeuLeuLeu 2811 3GCCTCCACTGGGGTGCAGACCGAG 2495 rTyrArgGluLysLeuThrSerLys 2831 GGCTGTGTTCATTCGCAAATCCTTC 2555 rGlnIleLeuGluGluLeuLysLys 2868 SCTCACCATGAGGAAGTCTTGGATT 2681 :||| nLeuGluGluGluLysGlu----- 2906 TCCGCAGGAGAAGGGCCCAGGCCA 2741 AGCACCAAAGCAGGGCCAGCCCTA 2801 ||| || || ::: ----GlnLysThrGlyThrValMet 2928 SAACAGCACTGCCACCTGGAGATC 2852 : sGluLeuLysGluThrLeuGluGlu 2948 STCGCAAAAGCCCAAAAGTGCAGAT 2978 |||::::::: -SerLysGlnAspSerArgGlySer 2996 GTCACGATTACTACTATTTCCAGA 3035 nSerSerTyrLygAsnLeuGluAsn 2691 ...... 2885 CysSerLeuLeulleSerHisGlu 2968 

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US-10-788-793-1 (1-4364) x PCT-US95-16216-1 (1-3248)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 -----
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-404
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                        1.17e-21
436.50
36.27%
20.61%
5.65%
                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                               ; ANTI-SENSE: NO PCT-US95-16216-1
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No.
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                                        LeuSerSerGlyGlnAsnLysAlaSerGlyLysArgGlnArgSerSerGlyIleTrpGlu 3036
                                                                      3096 ATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCAAATCTCCAG 3155
                                                                                                                              3036 GAGAAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCATCCCCCATCCAA 3095
                                                                                           :||| ::: |||:::|
3054 sLysAlaValMetSerGlyIleHisProAlaGluAspThrGluGlyThrGluPheGluPr 3074
                                                                                                                                                                                                             :||] ::::::
3094 rProTyrIleLeu-----ArgArgThrThrMetAlaThrArgThrSerProArgLe 3111
                                                                                                                                                                                                                                                                                                                                                                                        3168 lAsnAsnLeu------ProGluArgSerProThrAspSerProArgGluGlyLeuAr 3185
                                                                                                                                                                                         -----CCGTGCGGAAGTACAAC 3233
                                                                                                                                                                                                                                                                                                            -----TGGGTTCTCAGTTTAAGCGATCTC---CTGGGCCTGCCGCTGAAGGCGTGAAGC
                                                                                                                                                                                                                                                                                                                           3111 uAlaAlaGlnLysLeuAlaLeuSerProLeuSerLeuGlyLysGluAsnLeuAlaGluSe 3131
                                                                                                                                                                                                                                                                                                                                                                     CCAGTTATCACCGTCCGGCCTGTCAACGTGACAGCGGAGAAGGAGGTTTCTACAGGCACA 3392
                                                                                                                                                                                                                                                                                                                                                                                                                           3393 GICCTICGCICTCCCAGGAACCACCICTTTCAAGACCCGGIGCTAGCAAAGIGACCAGC 3452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3453 ACTATAACTATAACCCCGGTCACAACGTCATCCACACGAGGAACCCAATCAG---TGTCA 3509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6

FORT-US95-16216-1

Sequence 1, Application PC/TUS9516216

GENERAL INFORMATION:

APPLICANT: Yen, Timothy J.

TITLE OF INVENTION: Nucleic Acid Encoding a Transiently

TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use

TITLE OF INVENTION: Expressed Kinetochore Protein, and Methods of Use

CORRESPONDENCES: 4

CORRESPONDENCE ADDRESS:

CORRESPONDENCE NAME: Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                   TCCAATGCTAATATCATCACCACGGAAGACAATAAAATTCACATTCACC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
CITY: Philadelphia Street Suite 720
CITY: Philadelphia STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DAP C Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3510 GGACAAGATGGGTCATCTCAGCGGCCTACCCCCACCC 3546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::||| ||| ||| 3185 gValLysArgGlyArgLeu-----ValProAlaPro 3195
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,700
FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
                                          3017
                                                                                                                                                                                      3216
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|841 CysIleSerGluLeuSerPheSerGlyProAsnAlaLeuValProMetAspPheLeuGly 1860
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|1881 ArgleubeuHisVallleGluAspArgAspArgLysValGluSerLeubeuAsnGluMet 1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1766 SerCysAspIleSerLysGluHisThrSerGluThrThrGluArgThrProLysHisAsp 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::
1786 ValHisGlnIleCysAspLysAspAlaGlnGlnAsp---LeuAsnLeuAspIleGluLys 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1861 AsnGlnGluAspIleHisAsnLeuGlnLeuArgValLysGluThrSerAsnGluAsnLeu 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 GAG---GCACACTATGGATCTGCAGAACCTGAGAAAGTGCTTCGGGTCCTGCACCGA--- 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AAAAAGACTAAGAAGTCTGTGGAGTTATCCAAGGAGGACCTCATCCAGCTCCTGAGTATC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 CGAGAAGATGTCATCCAC----ATGCTGAGGACAGAGAAAACCAAGCCCGAGGTTCTG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                525 GACAGACTGGAGGAAAAGCAGAAGGAGACGTACCGCCGCTGCTAGAGCAGCTGCTGCTG 584
                                                                                                                                                                                                                                  51 TTAAGGAGTCGACAACAGGTGGGAATGAGATCACGAAAT-----CAAGGTGGAGAAAGT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                        156 GGTGGTAAGGGCCCCTCAGAAGATGCAAAAAAAAAAGACAAGGCCAATCGGAAGGAGGAGAT
                                                                                                                                                                                                                                                                                                                                      105 TCA-----TCTAACGGGCATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 GTCATGGCTTCCGGAACTATCAAAAGGCACCTCAAACCATCTGGAGAA-----AGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 GCTGAGAAGTGTCACAGGCGCACCGTGTACGAGCTGGAGAACGAGAAGCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 ATCCTTGCTCAAGAGAGAGTCCATAGGAGAAGACGTCTATGAGAAACCTATCTCAGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 ATGGAAGGGGAGTTGCAG------
3248
316
240
527
450
63
  Length:
Matches:
Conservative:
Mismatches:
Indels:
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350

1920

464

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1990 716 2010 737 2030 770 2050	806 2070 836 2090 848 2110 908	2146 1028 2162 1073 2181 1079 2201 1133 2221	224 7 230 231 232 233 233 233 234 234 234 234 234 234
1971	771	909 GAAAACTCAAAGCGCTCACTTACAAATCCAAGGAAGACCGCCAGAAGCTCCTCAAGTTA 2131 GluLyBleuGlnSerLeu	
B & B & B & B.	6 8 6 8 6 8 8	8 8 8 8 8 8 8 8 8 8 8 8	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

1425	CTCCATCTGAACCTGGAGAAGGAGAAGAACCTAACCAAAGACCTGCTGAACGAGCTG 1481 ::: :::::       ::     AlaGluIleGlnIleLysGluGluSerLysThrAlaValGluMetLeuGlnAsnGlnLeu 2361
1482	GAGGTGGTCAAGAGTCGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCC 1541
1542	ThrGluGlnSerLeuAspProProlleGluGluGluHisGlnLeuArgAsnSerIleGlu 2400
1569	AAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGAGAAAATATGATGGAG 1622         ::::::::::::::::::::::::::::
1623	AAAATAAAGCAAGAAGAGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAGCAG 1682
1683	hrAsnGln
1713	ATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAATCTGAA 1751 
1752	ATGGAGAAAAGGAGTACAGTCTGACAAAGGAGGAT 1790 :::       :::::         :::::
1791	GAGCTGATGGGTAAACTGAGGAGGAAGAAAGGTCCTGTGAACTG 1838
1838	1838
2512	SerSerPheGluAsnIleLeuGlnGluLysGluGlnGluLysValGlnMetLysGluLys 2531
1839	GGCA : Glul
1893	AGGGAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTC 1934
1935	ACCTGCCCGGAA
, 6	GACAAT 195
2592	TyrileValLeuGlnSerSerValLygGlyLeuIleGlnGluValGluAspGlyLygGln 2611
1953	AAGATCAGAGAACTAACGCTTGAAATCGAGACTCGAAGAACGGCTCCAGCAGTTGGAG 2012
2013	GTGGTGGAGGGGGACTTGATGAGACCGAGGACGAATATGAC
2055	
2091	GCAAACTTCCTCTCCCAGCAGCTCGAGGAAATCAAACAC
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CTGAGAGAGAAAATTGCCAAAGGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAG 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1443 AAGGAGAAGAACCTA-----ACCAAAGACCTGCTGAACGAGCTGGAGGTGGTCAAGAGT 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1497 CGAGTTAAAGAACTCGAATGCTCCGAGAGTAGACTGGAGAAGGCCGAGTTAAGCCTCAAA 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1557 GATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGGGAAAATATG 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCACCTGCCCGGAAGACAATAAGATCAGAGAACTAACGCTTGAAATC------ 1979
                                                                                                                                                                                                                                                                   1215 AGTCTGCGCAAGCGCGTGCTTGAGATGGAGGGCAAGGATGAAGAGTCACGAAGACGGAG 1274
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                                                           670 GlnGlnGluArgArgGluGlnArgLeuLysArgGluGluGluGluGluArgLeuGluGln 689
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|GluLysSerGluArgGlnArgLeuSerAlaArgProProLeuArgGluGlnArg 812
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                                                                                                                                                     -----GAGCTGGAAGACCAATAAAAGCCTTCAGAAGGCAGAAGAGCTCCAGGAG
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                                                                                              CGACTCAAACTG-----GTTGGCTTATCGCAAAGGATTGAG-----
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| ArgGluGluGludRgArgAspTrpLeuLysArgGluGluGluThrGluArgHisGlu 487
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|LeuLysLeuGluGluGluGluArgArgGluGlnGlnGlnGlnArgArgGluGlnGlnLeuArg 527
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Matches:
Conservative:
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Indels:
          TELEFAX: (714) 766-9502
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amino acids
 (714) 760-0404
                                                                                                                                                3.17e-21
429.00
41.20%
23.18%
5.55%
                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-056-200-94
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Query Match:
DB:
                                                                                                                                                                              Percent Similarity:
TELEPHONE:
                                                                                                                                       Alignment Scores
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364 LeuArgArgGluGluGluGluArgArgGluGlnGlnLeuArgArgGluGlnGluGluGlu 383
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216
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                                                                                              STATE. CACOUNTRY: U.S.A.

ZIP: 39660.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC Compatible
COMPUTER: TBM FC Compatible
COMPUTER: TBM FC Compatible
COMPUTER: TBM FC Compatible
COMPUTER: TBM FC COMPACH
COMPUTER: TBM FC COMPACH
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COMPUTER: TBM FC COMPACH
SYSTEM: TBC COMPACH
FILING DATE: 130-APR-1997
FILING DATE: 30-APR-1997
FILING DATE: 30-APR-1993
ATTORNEY AGENT INFORMATION:
NAME: Fedrick, Michael F
REGESTRATION NUMBER: JACACH
TELECOMMINICATION NUMBER: MIHOS4.001A
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TITLE OF INVENTION: Mehods of Using Same
MOMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: & G20 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
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Mismatches:
Indels:
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Matches:
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TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1898 amino acids
TYPE: amino acid
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429.00
41.20%
23.18%
5.55%
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Best Local Similarity:
Query Match:
DB:
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1072 GluLeuGlnGluGluGluGlnLeuLeuGlyGluGluArgGluThrArgArgArgGln 1091
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1163 LeuGlnArgGlnLysArgLysGlnArgTyrArgAspGluAspGlnArgSerAspLeuLys 1182
                                                      933 GluGluArgGluLysArgArgArgGlnGluGlnGluArgGlnTyrArgGluLyGluGluGln 952
                                                                                                                                                                                           TrpGlnLeuGluGluGluArgLysArgArgArgHisThrLeuTyrAlaLysProAlaLeu 912
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Patent No. 2958752
GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Chung, Soo-11
APPLICANT: Chung, Soo-11
APPLICANT: Thung, Soo-11
APPLICANT: Parks, Soo-11
APPLICANT: Parks, Soo-11
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
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US-08-800-644-94
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468 ArgGluGlnGluArgArgAspTrpLeuLysArgGluGluGluThrGluArgHisGlu 645 GACTACATGAACAAGAGGACGACTTCACCAACTGGAGGAGGAGGAGGGTTG 645 GACTACATGAACAAGAGGACGACTTCACCAACTGGAGGAGGAGGAGGGTTG 648 GlnGluArgArgLysGlnGlnLeuLysArgAspGlnGluGluGluArgArgGluArgTrp 705 AAAAAGCTCCTTGAACAAGAAAAAGCTTACCAAGCCCGCAAAGAAAAAGGAAAAGCTAAG 668 LeuLysLeuGluGluGluGluArgArgGluGlnGlnGlnGlnGlnGlnEeuArg 669 LeuLysLeuGluGluGluArgArgGluGlnGlnGlnGlnGlnGlnEeuArg	un oo	825 GACGAGAGGCAGATGCACATCGAGCAACTGGGGCCTGCAGAGTCAGAAAGTCCAGGACCTC	885 ACTCAGAAGCTGAGGGAGGAAGAAAAACTCAAAGCGGTCACTTACAAATCCAAGGAA	945 GACCGCCAGAAGCTGCTCAAGTTAGAAGTGGACTTCGAACACACAGGCCTCGAGGTTTTCC       :::       :::	1005 CAGGAGCACGAAGAGATGACGCCAAATTGGCGAATCTAAGAATCTCACAACCGGCAACTT :::	1065 CGACTCAAACTGGTTGGCTTATCGCAAAGGATTGAG	1101GAGCTGGAAGAGACCAATAAAAGCCTTCAGAAGGCAGAGGAAGAGGCTCCAGGAGGGGGGGG	1155 CTGACAGAGAAAATTGCCAAAGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAG	1215 AGTCTGCGCAAGCGCGTGCTTGAGATGGAGGCAAGGATGAAGAGATCACGAAGACCGAG	1275 GCCCAGTGCCGGGGGGTGAAGAAGAAGTCCCAAGAAGAACACCACAGGAAGCTT	1335 AGACTAGAAGTGGAGAAGCTGCAGAÀGAGGATGTCTGAGCTGGAGAAG	1383 CTGGAGGAAGCGTTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTGAACCTGGAG	1443 AAGGAGAAGACCTAACCAAAGACCTGCTGAACGAGCTGGTGGTGGAGGTGGTCAAGAGT	1497 CGAGTTAAAGAACTCGAATGCTCCGAGAGAAGACTGGAAGAGGCCGAGTTAAGCCTCAAA :::	1557 GATGACCTTACAAAGCTGAAGTCCTTCACTGTGATGCTGGTGGATGAGAGAAAAATATG
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2298 CAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGA-----TTTATGGAAGAAGAA 2348 2429 2430 AGGCCGAGTGGGAACGCCGAAGGATGGTGGACGTGCCTGTGGCCTCCACTGGGGTGCAG 2489 2082 -----CAGGATAAGGCAAACTTCCTCTCCCAGCAGCTCGAG--------GAG 2120 2175 CAGGAAGCCGAACTGCGACACAGGTTTCGGCTGGAGGAGGCTAAAAGTCGTGAT---- 2228 :::||| ||| ||| ||| ||| ::: 993 GluGluProGluLysArgArgArgArg---GlnGluArgGluLysLysLyrArgGluGluGlu 1011 1111 1092 GluLeuGluArgGlnTyrArgLysGluGluGluGluGlnGlnGluGluGluGluGluGluLeuLeu 1111 2490 ACCGAGGCGGTGTGCGGGATGCTGCGGAGGAGGAGACCCCGGCTGTGTTCATTCGCAAA 2549 1725 AAGAAGCTTTTAAAACTCAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGAG 1784 1980 ---GAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGGGGGACTTGATGAAG 2036 2037 ACCGAGGACGAA-----TATGACCAGTTGGAGCAGAAGTTCAGAACCGAG---- 2081 2121 ATCAAACACCAAATGGCCAAGCACAAAGCCATAGAGAAAGGGGAG-----GCCGTGAGC 2174 2229 -----TTACAGGCCGAGGTGCAGGCTCTCAAGGAG------TTACAGGCCGAGGCTCTCAAGGAG------ 2258 1112 ArgGluGluProGluLysArgArgArg-----------GlnGlu 1122 1668 TTTAAGGTGGAGCAGGGAAAAGTC---ATGGATGTGACGGAAAAGCTAATCGAGGAAAGC 1724 1785 AGGGAT---GAGCTGATGGGTAAACTGAGGAGCGAAGAAGAAGGTCCTGTGAACTGAGC 1841 1875 GGCATA---GAGGAGGTAGAAAGGGAAATAAACCGAGGTAGGTCGTGCAAGGGGTCTGAG 1931 ::: :::||| ||| 1072 GluLeuGlnGlnGluGluGlnLeuLeuGlyGluGluArgGluThrArgArgArgGln 1091 1617 ATGGAGAAAATAAAGCAAGAAGAGAGAAAGTGGAT------GGGTTGAATAAAAC 1667 ||| |||:::|||::: 793 GlulysSerGluArgGlyArgGlnArgLeuSerAlaArgProProLeuArgGluGlnArg 812 ::: |||::::::||| 853 GluGluGluGluLeuGlnArgArgGluArgAlaGlnGlnLeuGlnGluGluGluAep 872 873 GlyLeuGlnGluAspGlnGluArgArgArgAlnGluGlnArgArgAspGlnLysTrpArg 892 2376 ----GICCICAAICIGACCAAGGAGCIAGAGCITICCAAGCGCIACAGCCGAGCTCIC 1932 TTCACCTGCCCGGAAGACAATAAGATCAGAGAACTAACGCTTGAAATC------2259

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	RESULT 9 US-09-914-259-11 Sequence 11, 94911cation US/09914259 Sequence 11, 949336 Datent No. 6495336 GENERAL INFORMATION: APPLICANT: Makowski, Lee APPLICANT: Williams, Mark TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES FILE REFERENCE: 8\$71-010-999 CURRENT APPLICATION: 2000-11-21 NUMBER OF SEQ ID NOS: 180 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11 LENGTH: 3878 TYPE: PRT CRANISM: Home sapiens GRANISM: Home sapiens	Length: 3878   Matches: 248   Conservative: 194   Mismatches: 367   Indels: 331   Gaps: 194-259-11 (1-3878)   He   He   He   He   He   He   He   H	Db 1676 GludinthrPhellysGluLysGluSparaphysProcludagbyalPro-Procl 1694  Oy 231 ACTACAAAAGGCACCTCAAACCACTGAGAAAAAAAACTAAGAAGTCT 287  Db 1694 ulieLeuSerAenGluArgTyralaleuGluLysAlaAenAsnAkrgLeuLeuLysIleLe 1714  Oy 288 GTGGAGTTATCCAAGGAGGCTCTCACCAGTACTGAGTATCATGAAAGGGAGTTGCAG 347  Db 1714 uLeuGluValValLysFhrThrAlaAla-ValGluGluThrIleGlyArgHisValLeuG 1734  Oy 348 GCTCGAGAAGATGTCATCCACAGGCGAGAAACCAAGCCGAGGTTCTGAG 407  Db 1734 1y

	AAGAAGCTCCAAGAGAAGAACACCAC 1322	Ŝ	
		qu	2489 AlaLysAspLeuGluLeuThrGlnCysTyrLysGlnIleLys
	215	ò	
1323 YD	13.23AGCAAGGAACTTAGACTTAGAAGTGGAAAAGTGGAAAGAAGAAGAAGAAGAAGAAG	qq	2509 GlnPheGluThrGluMetLeuGlnLysLysIleValAsnLeu
	, ,	ò	2082 CAGGATAAGGCAAACTTCCTCTCCCAGCAGCTCGAGGAA
	1350	ąg	::: 2529 LysvalAlaAlaLeuvalSerGlnIleGlnLeuGluAla
	149	, &	2139 AAGCACAAAGCCATAGAGAAAGGGGAGGCCGTGAGCCAGGAA
	ysGlu	qq	2548LysPheCysGlnAspAsnGlnThrileSerSerGlu
1494		ò	2199 TITCGGCTGGAGGCTAAAAGTCGTGATTTACAGGCCGAG
2219		q	2566 GlnAsnLeuAsnGlnLeuArgGluAspGluLeuGlySerAsp
1548		ò	2259 AAGATCCACGAGCTG
		qq	2586 ArglieSerdluLeuGluSerGlnValValGluMetHisThr
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	PheAlaGlnIleIleGlnGluLvgGluVal	qq	2606 GluGlnValGluIleAlaGluLysAsnValLeuGluLysGlu
	- AAGGTGGAGCAGGAAAGTCATGGATGTG	ò	2304 CAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAAGAA
		q	LysLysGlnArgGlu
		ò	2364 AIGGGGAGGICCTCAAICTGACCAAGGAGCIAGAGCIT
	spLeuGluThrGlnIleGlu	q	GlnAspValĠĺuŸa
Qy 1740	CTCAAATCTGAAATGGAGGAAAAGGAGTACAGTCTGACA 1778	λö	2421CGAGCTCTCAGGCCGAGTGGGAACGGC
2312		අු	2666 PhePheAsnGluLeuGluAlaLeuArgAlaGluSerValAla
Oy 1779 AAG		ò	2466 CCTGTGGCCTCCACTGGGGTGCAGACCGAGGCGGTGTGCGGG
::: Db 2329 Glu	:::::: :::   :::::	qa -	
Oy 1818	GAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTAAAGAAGCGGCTTGAT 1874	ò	
Db 2349 Thr	ThrSerMetAsnAlaHisSerLeuSerGluGluAlaAspSerLeuLysHisGlnLeuAsp 2368	qo ,	
Qy 1875 GGC	GGCATAGAGGAGGTAGAAAAAGGGAAATAAACCGAGGTAGGGTCGTGCAAGGGGTCTGAGTTC 1934	ò ·	CTTCGACAGGTAGG
Db 2369 Val	::: ::: ::: 2369 ValVallleAlaGluLysLeuAlaLeuGluGlnGlnValGluThrAlaAsnGluGluMet 2388	QQ	
Qy 1935 ACC	AGA	RESULT US-08-	10 714-741-41
(     Db 2389 Thr		; Seque	Sequence 41, Application US/08714741 Patent No. 6500613
Qy 1977 ATC	1977 ATCGAGAGTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGG 2024	; GENI	avid E.
::: Db 2409 Leu	:::        :: :: :::		PPLICANT: McDaniel, Larry S. PPLICANT: Swiatlo, Edwin
Qy 2025	GACTTGATGAAG 2036		PFLICANT: Yother, Janet PFLICANT: Crain, Marilyn J. DD:TCANT: H.Jlincahosa Susan
Db 2429 Ser	SerValAsnValAlalleAspHisLeuSerLysAspLysProGluLeuGluValValLeu 2448	- A	PPLICANT: Tart, Rebecca PPLICANT: Tart, Rebecca PPLICANT: Alexia
	ACCGAGGACGAATATGACCAGTTGGAG		TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM,
Db 2449 Thr	2449 ThrGluAspAlaLeuLysSerLeuGluAsnGlnThrTyrPheLysSerPheGluGluAsn 2468		TITLE OF INVENTION: PORTIONS AND PRODUCTS NUMBER OF SEQUENCES: 47
Qy 2063	2063		DENCE ADDRESS

AAGAAACTAAGAACAAGAAC 2363 ::||| || || /8Gluly8Ly8ArgSerPro 2645 ||| | BSerAsnGluGluSerGly 2665 THEREOF, 1, AND USES OF SUCH GENES, BABPMetGlnGluGlnGly 2508 --CAGAAGTTCAGAACCGAG 2081 AAATCAAACACCAAATGGCC 2138 :::::: taValGlnGluTyrAla--- 2547 AGCCGAACTGCGACACAGG 2198 | ||| .uProGluArgThrAsnIle 2565 GGTGCAGGCTCTCAAGGAG 2258 :::: plleSerAlaLeuThrLeu 2585 rrSerLeulleLeuGluLys 2605 AGACCAGCTGTCTCAGCTC 2303 TŢĊÇAAGCGCTACĄĠÇ--- 2420 CCGAAGGATGGTGGACGTG 2465 ::: aThrLys-----Ala 2682 GGATGCTGCGGAGGAG 2525 ::: .uGluLeuLeuValLysGlu 2702 AAATÇAÇATCATGAGTAAT 2582 nLeuGluSerThrValSer 2488 \_\_\_\_\_ 2273 :::||| gAspHis-----2718 

	AGCGAGAAAGAAGCCGGCAGCTGAGCTTACTAAAGAAGAAGCGGCTT AGCGAAGAAAGAAAGAAGCTCTGAACAAGAAGAAGCGGCTT
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Oy 3060 AGCGCCTTTGCC  Db 727 GluAspTyrAla  QY 3120 GCTCCCACTGAA  (Y) 3120 GCTCCCACTGAA  (Y) 3162 CCTATGGGA  Db 759 GlyMetTTPTyr  (QY 3171AGGACTATC  Db 779 TyrAsnArgLeu  (1:10)	Oy 3228  Db 799 ThrGlyTrpLyse  Oy 3252 ACCACGGAAGAC  ::::::  Db 818GlnAsn  RESULT 11  US-09-310-187-1  : Sequence 1, Application 1; Patent No. 6358751  ; Patent No. 6358751  ; GENERAL INFORMATION:  ; APPLICANT: Bedoseyeva,  ; TITLE OF INVENTION: In;  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.  ; TITLE OF INVENTION: Gr.	## WOUNDER OF SENT LD NOST   ## SEQ ID NO 1 ## LENGTH: 1939 ## TYPE: PRT   ## ORGANISM: Homo sapiens   ## US-09-310-187A-1   ## Alignment Scores:   ## Fred. No ::	Qy       177 GATGCAAAAAAG         Qy       177 GATGCAAAAAAG         Bb       918 GlualaLysvall         Qy       228 GGAACTATCAAA         Qy       288 GTGGAGTTATCC         Qy       288 GTGGAGTTATCC         Db       950 SerGluLeuLysl         Qy       342 TTGCAGGCTCGA         Qy       342 TTGCAGGCTCGA         Qy       342 TTGCAGGCTCGA         Qy       342 TTGCAGGCTCGA         Qy       344 TTGCAGGCTCGA         Qy       384
GludanGlnValHisArgLeuGluGlnGluLeuLysGluIleAspGluSerAspSerGlu TTGATGAAGACCGAGGACGAATATGACCAGTTGAGGCAGAAGTTCAGAACCGAGCAG		2541 ATTGGCAAATCCTTCCAGGAGAAATCACATCATGAGTAATCTTGGACAGGTAGGCCTG 2600	2772 GTCCTAGCACCAAAGCAGGCCCGACACATCCGTGTACACCAGATCATGAGAAC 2831 660AlaProAlaProAlaProGluLysPro
8 6 8 6 8 6 8	8 6 8 6 8 6 8 6 8 6 8	8 6 8 6 8 6 8	8 6 8 6 8 6 8 6

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GGACAGGCCTGCATCCCAAATCATGACGGTGTCAACATCTGCA 3119
                                                       AATCGCTGTCTCCTGAATCT---------CAGGAAGTG 3161
                                                                                                                                                                                                                                                                                       CAATAAAATTCACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGG 3311
                                                                                                                                                                                                                                 ------3251
                            ----- 738
                                                                           : ||| :::||||||| sProAlaProTysThrGlyTrpLysGlnGluAsn 758
                                                                                                                                           rPheTyrAsnThrAspGlySerMetAlaThrGlyTrpSerGluGluGlu 778
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nAsnGlySerTrpTyrTyrLeuAsnSerAsnGlyAlaMetAlaThrGly 835
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|||shiyayalbyayanbeuThrGluGluMetAlaGlyLeuAspGlu 989
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Qy 1293 AAGAAGAAGCTCCAAGAGGAAGAACA ::::::: Db 1346 ArgGluGlnTyrGluGluGluThrGl	1340	1341	1395 1406	1455 CTAACCAAAGACCTGCTGAACG :::      ::: : 1426 GluileGluAspLeuMetValA	1446 LysLysGlnArgAsnPheAspL	OY 1521 GACAGIAGACIGGAGAAC 	Qy 1572 CTGAAGTCCTTCACTGTGATGCTGGTC       ::: Db 1486 LeuLy8AsnAlaTy;	Oy 1632 CAAGAAGAGAGAAAGTGGATGGGTTV	Qy 1692 ATGGATGTGACGGAAAAGCTAATCGACDA 1512 SerAspLeuThrGluGlnLeuGlyGl	Oy 1734TT)  Db 1532 ArgLysGlnLeuGluValGluLysLe	Oy 1770 AGTCTGACAAAGGAGAGATGAGCTV	1812 AGCGAAGAAGAAGGTC :::          1572 AlaGluIleGluArgLy	1833	Qy 1857TAAAGAAGCGGCTT :::      :::: Db 1612 GluValLeuArgValLysLysEysMe	Qy 1902 AACCGAGGTAGGTCGTGCAAGGGGTCT :: Db 1632 SerHisAla	Oy 1962 GAACTAACGCTTGAAATCGAGAGACTC	Oy 2022 GGGGACTTGATGAAGACCGAGGACGA     :::::      :::::  b 1660 AspAspAlaValArgAlaAsnAspAsg
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990 IleIleAlaLysLeuThrLysGluLysLysAlaLeuGlnGluAlaHisGlnGlnAlaLeu 1009 426 GAACCTGAGAAAGTGCTTCGGGTCCTGCACGAGATGCCATGCTTGCT	1010 AspaspreducinvalGindiuasprysvalasnserreuserrysser 1025 486 ATAGGAGAAGACGTCTATGAGAACCTATCTCAGAGCTGGACAGACTGGAGGAAAG 542 1026LysvallysereudiudindinolinvalAspaspseudiudiyserfeudiudindiu 1043	543 CAGAAGGAGACGTACCGCCGCATGCTAGAGCAGCTGCTGCTGGT 587 ::	588 GAGAAGTGTCACGGCACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACTGAC 647	•	708 AAGCTCCTTGAACAAAAAGCTTACCAAGCCCGCAAAGAAAAGGAAAACGCTAAG 764	765 CGGCTCAACAAACTTCGAGATGAGCTTGTG 794	795 AAGCTCAAGTCCTTGGCCCTCATGTTGGTGGAGGGGGGGG	855 GGCCTGCAGAAAGTCCAGGACCTCACTCAGAAGCTGAGGGAGG	1156 GIYGLYALBININESETVALGINILGGIUMGCASRLYSELYSELYSEATGGIUATGGIULNGS 1175   1175   1175   1175   1175   1175   1175   1175   1176   1177   1	GAACACAAGGCCTCGAGGTTTTCCCAGGAGCACGAAGAGATGAACGCCAAATTG	GCGAATCAAGAATCTACCAA 9179179179179179179179179179179179179179	CTTCGACTCAAACTGGTTGGCTTATCGCAAAGGATTGAGGAGCTGGAAGAGACCCAATAAA	1122 AGCCTTCAGAAGGCAGAGGAAGAGCTCCAGGAGCTGAGAGAAATT 1169 :::	1170GCCAAAGGGGAATGTGGA 1187           ::   ::			129
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2081	2. GGGGACTTTGARGACCGAGGACGAATATGACCAGTTGGAGCAGAAGGTCCAGAG	202
2021	2 GAACTAACGCTTGAAATCGAGAGACTGAAGAAACGGCTCCAGCAGTTGGAGGTGGTGGAG 	196
1639	::: 2 SerHisAlaAsnArgMetAlaAla	163
1961	2 AACCGAGGTAGGTCGTGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGA	190
1631	:::       ::::        ::::::::::::::	161
1901	7CTAAAGAAGCGGCTTGATGGCATAGAGGAGGTAGAAAGGAAATA	185
1611	 2 HisGlnArgValValAspSerLeuGlnThrSerLeuAspAlaGluThrArgSerArgAsn	159
1856	3	183
1591	:::	157
1832	2 AGGGAAGAAAGGTCCTGT	181
1571	   SerLeuGluHisGluGluGlyLysIleLeuArgAlaGlnLeuGluPheAsnGlnIleLys	155
1811	0 AGTCTGACAAAGGAGAGAGGATGATGGGTAAACTGAGG	177
1551	2 ArgiysGlnLeuGluValGluLysLeuGluLeuGluSerAlaLeuGluGluAlaGluAla	153
1531	2 SerAspieuthrGluGinLeuGlyGluGlyGlyLysAsnValHisGluLeuGluLysVal	151
1733	2 ATGGATGTGACGGAAAAGCTAATCGAGGAAAAGCAAGAAGCTT	169
		150
1691	2 CAAGAAGAAGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAGGAGGAAAAAGTC	163
1631	572 CTGAAGTCCTTCACTGTGATGCTGGTGGATGAGAGAAAAATATGATGGAGAAAATAAG 163          :: 186 LeulysasnAlatyrGluGluSexIeuGluHisbeuGluthrPhelys 150	157
1485	:::      GlnSerGluLeuGluSerSerGlnLysGluAlaArgSerLeuSerThrGluLeuPheLys	146
1571	1 GAGAGTAGACTGGAGAAGGCCGAGTTAAGCCTCAAAGATGACCTTACAAAG	152
1465		144
	5	148
1445	6 GlulleGluAspLeuMetValAspValGluArgSerAsnAlaAlaAlaAlaLeuAsp	142
1484	5 CTAACCAAAGACCTGCTGAACGAGCTGGAG	145
1425	6 ValGluAlaValAsnAlaLysCysSerSerLeuGluLysThrLysHisArgLeuGlnAsn	140
1454	5 TTCAGCCGGAGTAAGTCGGAATGCACCCAGCTCCATCTGAACCTGGAGAAGGAGAAGAAC	139
1405	6 GluGluLeuGluGluAlaLysLysLysLeuAlaGlnArgLeuGlnAspAlaGluGluAla	138
1394	1GAAGTGGAGAAGCTGCAGAAGAGGATGTCTGAGCTGGAGAAGCTGGAGGAAGCG	134
1385	6 AlaAsnSerGluValAlaGlnTrpArgThrLysTyrGluThrAspAlaIleGlnArgThr	136
1340	0	134
	6 ArgGluGlnTyrGluGluGluThrGluAlaLysAlaGluLeuGlnArgValLeuSerLys	134
1340	3 AAGAAGAAGCTCCAAGAGGAAGAACACCACAGCAAGGAACTTAGACTA	129

Best Local Similarity: 19.51% Mismatches: 583 Query Match: 5.30% Indels: 377 DB: 59	US-10-788-793-1 (1-4364) x US-08-466-390-4 (1-2101)	Qy 51 TTAAGGAGTCGACAACAGGTGGGAATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCT 110	Db 680 LeuArgSerGluGlnGlnLysAlaThrGluLysGluArgValAlaGlnGluLysAspGln 699	Oy 111AACGGGCATGTCTCCTGCCCCAAGTCCTCCATCATCAGCAGTGATGGTAAGGGC 167	Db 700 LeuGlnGluGlnAlaLeuLygGluSerLeuLygValThrLygGly 716	Qy 168 CCCTCAGAAGATGCAAAAAAAAAAAAAAAAAAAAAAAAA	Db 717 SerLeuGluGluGluLysArgArgAlaAlaAspAlaLeuGluGluGluGluArgCysIle 736	Qy 228 GGAACTATCAAAAGGCACCTCAAACCATCTGGAGAAAAGTGAGAAAAAGGACTAAGAAGTCT 287	Db 737 SerGluLeuLysAlaGluThrArgSerLeuValGluGlnHisLysArgGluArgLysGlu 756	Qy 288 GTGGAGTTATCCAAGAGGAC	Db 757 LeuGluGluGluArgAlaGlyArgLyBGlyLeuGluAlaArgLeuLeuGlnLeuGlyGlu 776	Qy 327 ATCATGGAAGGTGGAGTTGCAGGCTCGAGAAGATGTCATCCACATGCTGAGGACAGAG 383	Db 777 AlaHisGlnAlaGluThrGluValLeuArgArgGluLeuAlaGluAlaMetAlaAlaGln 796	Qy 384 AAAACCAAG	Db 797 HisThrAlaGluSerGluCysGluGlnLeuValLysGluValAlaAlaTrpArgAspGly 816	Qy 405GAGGCACACTATGGATCTGCAGAACCTGAGAAAGTGCTT 443	Db 817 TyrGluAspSerGlnGlnGluGluAlaGlnTyrGlyAlaMetPheGlnGluGlnLeuMet 836	Qy 444 CGGGTCCTGCACCGAAGATGCCATCCTTGCTCAAGAAAGTCC 485	Db 837 ThrLeuLysGluGluCysGluLysAlaArgGlnGluLeuGlnGluAlaLysGluLysVal 856	Qy 486 ATAGGA	Db 857 AlaGlyIleGluSerHisSerGluLeuGlnIleSerArgGlnGlnAsnLysLeuAlaGlu 876	Qy 492 515	Db 877 LeuHisAlaAsnLeuAlaArgAlaLeuGlnGlnValGlnUysGluValArgAlaGln 896	Qy 516TCAGAGCTGGACAGACTGGAGGAAAAGCAGAAGGAGAGGAGGACGCCGCTG 566	Db 897 LysLeuAlaAspAspLeuSerThrLeuGlnGluLysMetAlaAlaThrSerLysGluVal 916	567CTAGAGCAGCTG	Db 917 AlaArgLeuGluThrLeuValArgLysAlaGlyGluGlnGlnGluThrAlaSerArgGlu 936	606 ACCGTGTACGAGCTGGAGAACGAGAAGCACAAGCACACACTACATG	Db 937 LeuVaiLysGiuProAlaArgAlaGlyAspArgGlnProGluTrpLeuGluGluGluGlnGln 956	Qy 654AACAAGAGGACGAC 668	Db 957 GlyArgGlnPheCysSerThrGlnAlaAlaLeuGlnAlaMetGluArgGluAlaGluGln 976	669 TTCACCAACCTGGAG		Qy 687CAGGAGGAGAGAGTTG 704	
Oy 2082 CAGGATAAGGCAAACTTCCTCTCCCAGCAGGAGAAATCAAA2126 :::	Oy 2127	Db 1697 ThrGluArgSerArgLysLeuAlaGluGluGluLeulleGluThrSerGluArgValGln 1716	Qy 2172AGCCAGGAAGCCGAACTGCGACAGGTTTCGGCTGGAGGCTAAAAGT 2222	Db 1717 LeuLeuHisSerGlnAsnThrSerLeuIleAsnGlnLysLysBetGluSerAspLeu 1736	Qy 2223 CGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAGAGAGA	Db 1737 ThrGlnLeuGlnSerGluValGluGluAlaValGlnGluCysArgAsnAla 1753	2283 GAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTTCAGCAAAGATTTATGGAA	Db 1754 GluGluLysAlaLysLysAlaIleThrAspAlaAlaMetMetAlaGluGluLeuLysLys 1773	2343 GAAGAAACTAAGAACAAGAACATGGGGAGGAGG	Db 1774 GluGlnAspThrSerAlaHisLeudluArgMetLysLysAsnMetGluGlnThrIleLys 1793	Oy 2382 AATCTGACCAAGGAGCTAGAG 2402	euGlnHisArgL	RESULT 12	Sequence Application US/08466390	ON:	TOUKAILI, GARX LIDGARD, GRAHAM P KIRIMITAN, MAKITI MITTONIAM CHIT MAND MARKEDO CHI	NOVEL MALIGNANT INTERIOR NUCLEAR · 6	CORRESPONDENCES: 0  CORRESPONDENCES: TEGYA. HURWITZ & THIBEAULT	125 HIGH S BOSTON	STATE: MA COUNTRY: USA	ZIP: 02110 COMPITTER PRADABLE FORM.	CONTOLER NEADABLE FORM:    MEDIUM TYPE: Floppy disk   Company tible   Company	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0. Version #1.25		FILING DATE: 06-JUN-1995	ATTORNEY/AGENT INFORMATION: , NAME: PITCHER ESQ, EDMUND R	; REGISTRATION NUMBER: 27,829 ; REFERENCE/DOCKET NUMBER: MTP-013	HS	; TELEFAX: (617) 248-7100 ; INFORMATION FOR SEQ ID NO: 4:	SEQUENCE CHARACTERISTICS:	umino acid	PE	nment Scores:	Pred. No.: 7.12e-20 Length: 2101	#CA.DO

10.7   CITALA ASPECTATION CONCENCE COMMON AND CONTROL OF STATES AND CONTROL OF STATES AND CONTROL OF STATES ASPECTATION CONT		1800 GGTAAACTGGAGAAGAAGGACCTGTGAACTGAGCTGCAGTGTAGACTTGTATA 1899 1848AlaGluGluAenArgGly	2085 GATAAGGCAAACTTCCTCCCCAGCAGCACAAATCAAACACCAAATGGCCAAGGCC 2144  [1531] GlnLy8LeuThrAlaGlnValGluGluLeuSerLysiceuAlaAspSer 1547  2145 AAAGCCATAGAGAAGGGGAGGCCGTGAGCCAGGAAGCCGAACTGCGACACAGGTTTCGG 2204  [1548]AspGlnAlaSerLy8ValGlnGlnGlnLysiceuJy8 1559  2205 CTGGAGGAGCCTAAAAGGTTTACAGGCCGAGGTGCAGCTCTCAAGGAAGAGTC 2264  [1560] AlaValGlnAlaGlnGlyGlyGluSerClnGlnGlnAlaGlnArgPheGlnAlaGlnLeu 1579  2265 CACGAGCTGATGAAAAGGAAGCCAGCTGTCAGCTCCAAGTCGACTCTT 2324  [157]	2325 CAGCAAAGATTATGGAAGAACTAAGAACAAGAACATGGGGAGGGGGGGG
105   MARAGCTCCTTGAACAAGAAAAGCTTAACCAAGCCCGCAAAGAAAAGGAAAACGCTAAG   1017   GinhlaapEechlaied	3 8 3 8 3 8 3 8 3	8686868686	8 8 8 8 8 8 8	8 8 8 8 8 8 8 8
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2013 ThrThrGluAlaGlnLysLysAlaAlaProAlaSerThrLysGlnAlaAspArgArgGln 2032
                                                                      2033 SerMetAlaPheSerIleLeuAsnThrProLysLysLeuGlyAsnSerLeu---LeuArg 2051
                                   ACCCCCACCCGCATTCCTATGTCAAAAGGTATGAAA
                                                                                                          3573 GCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAATCTGACCAAATTCCAGCCTCGA
                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08470950
Patent No. 5698439
GENERAL INFORMATION:
APPLICANT: TOUKANTIC, GARY
APPLICANT: LIDGARD, GRAHAM P
TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,950
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFRERENCE/DOCKET NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
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Conservative:
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YSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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1957 GlnProlleGlnIle---AlaGlu------GlyThrGlyIleThrThrArgGlnGln 1972
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1973 ArglysArgValSerLeuGluProHisGlnGlyProGlyThrProGluSerLysLysAla 1992
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1388 SerLysGlnAlaAlaGlyGlyLeuArgAlaGluLeuLeuArgAlaGlnArgGluLeuGly 1407	1686 AAAGTCATGGATGTGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAA 1745	1746   TCTGAAATGGAGGAAAAGGAGTACACTCTGACAAAGGAGAGGAG	GGTAAACTGAGGAGGAGAAGGACGTGTGAACTGAGCTGCAGTGTAGACTTACTA  GGTAAACTGAGGAGGAGGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTA  [		1917 TGCAAGGGGTCTGAGTTCACCTGCCCGGAAGACAATAAGATCAGAGAACTA 1967	ACGCTTGAAATCGAGAGACTGAAGAACGGCTCCAGCAGTTGGAGGTGGTGGAGGG	GlnArgGluAlaGlnSerThrAlaArgGluLeuGluValMetThrAlaLysTyrGluGly	<pre>2025 GACTTGATGAAGACCGAGACGAATATGACCAGTTGAAGCAGAACCGAGGAG 2084 :::    :::    :::    1515 AlaLysValLysValLeuGluGluArgGlnArgPheGlnGluGluArg 1530</pre>	GATAAGGCAAACTTCCTCCCAGCAGCTCGAGGAAATCAAACACCAAATGGCCAAGCAC	GINLY8LeuinrAlaGinvalGluGiuLeuserLy8Ly8LeuAlaAspSer	<pre>2145 AAAGCCAAAAAAAAAGGGAGGCCGTGAGCCAAAGGCGGAACTGCGACACTGCGACATTGCG 2204 1:1::: 1548AspGlnAlaSerLy8ValGlnGlnGlnGln</pre>	2205 CTGGAGGCTAAAAGTCGTGATTTACAGGCCGAGGTGCAGGCTCTCAAGGAGAAGATC 2264	1560 AlaValGinAlaGinGlyGlyGlyGluSerGlnGlnGluAlaGinArgPheGinAlaGinLeu 1579	2265 CACGAGCTGATGAACAAGGAAGACCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTT 2324 :::	2325 CAGCAAAGATTTATGGAAGAAGAACTAAGAACAAGAACATGGGGAGGGA		2385 CTGACCAAGGAGCTATACCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAAC 2444	1620 GinLeuArgSerLeuGluGlnLeuGlnLysGluAsnLysGluLeuArgAlaGluAla 1638	2445 GGCCGAAGGATGGTGGAGCTGTGGCCTCCACTGGGGTGCAGACCGAG 2495	ACCCCGGCTGTG	1657 GlnThrCygArgHisLeuThrAlaGlnValArgSerLeuGlu 1670	2556 CAGGAGGAAAATCACATCATGAGTAGTTCTTCGACAGGTAGGT	1671 AlaGlnValAlaHisAlaAspGlnGlnLeuArgAspLeuGlyLysPheGlnValAla 1689	2616 CGGTCCTCGGTCCTCGACAGGAATGACGAATGAGCTCACATGAGGAAGTCT 2675	1690 ThraspalaLeuLysSerargGluProGlnAlaLysProGlnLeuAspLeuSerIleAsp 1709	2676 TGGATTCCTTGGATGAGAAAAGAGAAAACGGTCCTTCCACTCCGCAGGAGAAAGGGCCC 2735 :::
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||| :::|||||| :::::: -----ThrThrArgSerSerAlaArgArgSerGlnAlaGlyVal------SerSer 1879 3216 CCCGTGCGGAAGTACAACTCCAATATCATCACCACGGAAGACAATAAAATT--- 3272 1899 GlnLeuAspAspTrpAsnArgIleAlaGluLeu-----GlnGlnArgAsnArgValCys 1916 2774 1749 LeubroProLysValGluSerLeuGluSerLeuTyrPheThrProlleProAlaArgSer 1768 1789 LysThrArgSerAlaArgArgThrThrGlnileIleAsnIleThrMetThrLysLys 1808 2919 CCAAGAATAACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCCAAAAGTGCAGAT 2978 1809 LeuAspValGluGluProAspSerAlaAsnSerSerPheTyrSerThrArgSerAlaPro 1828 ||| |1880 GlyAlaProProGlyArgAsnSerPheTyrMet---GlyThrCysGlnAspGluProGlu 1898 :::::: 1937 IleThrAspGluGluMetLysThrGlyAspProGlnGluThrLeuArgArgAlaSerMet 1956 |||::: ::: |||||| 1957 GlnProIleGlnIle---AlaGlu------GlyThrGlyIleThrThrArgGlnGln 1972 2979 CCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGAGAG 3038 3039 AAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCA---TCCCCCATCCAA 3095 |||||:: ||| |||| 1847 GlySerProAspTyrGlyAsnSerAlaLeuLeuSerLeuProGlyTyrArgPro----- 1864 3096 ATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAG 3155 -----CACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGC 3326 1917 ProProHisLeuLysThrCysTyrProLeuGluSerArgProSerLeuSerLeuGlyThr 1936 AGGAACCACCTCTCT-------TCAAGACCCGGTGCTAGCAAGTG 3446 ||| :::||| 1973 ArgiysArgValSerLeuGluProHisGlnGlyProGlyThrProGluSerLysLysAla 1992 |||||| |ThrSerCysPheProArgProMetThrProArgAspArgHisGluGlyArgLysGlnSer 2012 |||||||| ThrThrGluAlaGlnLysLysAlaAlaProAlaSerThrLysGlnAlaAspArgArgGln 2032 3573 GCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAATCTGACCAAATTCCAGCCTCGA 3632 --- CCTGTCAACGTGACAGCGGAGAAGGAGGTTTCTACAGGCACAGTCCTTCGCTCTCCC 3407 -----GTC 3473 3474 ACAACGTCATCCACACGAGGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGG 3533 CCT-------ACCCCCACCCGCATTCCTATGTCAAAAGGTATGAAA 3572 1729 ArgThrGlnProAspGlyThrSerValProGlyGluProAlaSerProIleSerGlnArg CTAGCACCAAAGCAGGCCAGCCCCTACACATCGTGACACCCAGATCATGAGAACAGC 2835 ACTGCCACCCTGGAGATCACAAGCCCCACATCTGAAGAGTTTTTC------2880 -------TCTAGTACCACCGTCATTCCTACCTTAGGCAACCAGAAA 3447 ACCAGCACTATA-----ACTATAACCCCG--------2736 AGGCCAAAC---CAGGGTGCAGGGCACCCCGGGGAGCTGGTC---2775 3408 3327 3351 1993 2013 3534 2033

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|037 AlaLeuAsnGluGlnArgValGluPheAlaThrLeuGlnGluAlaLeuAlaHisAlaLeu 1056
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| 077 IleLysGluLeu---GluGluLeuArgGlnThrValLysGlnLeuLysGluGlnLeuAla 1095
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LysLysGluLysGluHisAlaSerGlySerGlyAlaGlnSerGluAlaAlaGlyArgThr 1115
     SerGluLeuLysAlaGluThrArgSerLeuValGluGlnHisLysArgGluArgLysGlu 756
                                                                                            327 ATCATGGAAGGGGAGTTGCAGGCT----CGAGAAGATGTCATCCACATGCTGAGGACAGAG 383
                                                                                                              857 AladiyileGluSerHisSerGluLeuGlnIleSerArgGlnGlnAsnLysLeuAlaGlu 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               957 GlyArgGlnPheCysSerThrGlnAlaAlaLeuGlnAlaMetGluArgGluAlaGluGln 976
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877 LeuHisAlaAsnLeuAlaArgAlaLeuGlnGlnValGlnGYuSGluValArgAlaGln 896
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                                288 GIGGAGITAICCAAGGAGGAC-----------------CICAICCAGCICCIGAGI
                                                                                                                                                                                                              ------GAGGCACACTATGGATCTGCAGAACCTGAGAAAGTGCTT
                                                                                                                                                                                                                                                                    444 CGGGTC-------CTGCACCGAGATGCCATCCTTGCTCAAGAGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                            ------GAAGACGTCTATGAGAAACCTATC------
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                                                                                                                                                                             797 HisThralaGluSerGluCysGluGlnLeuValLysGluValAlaAlaTrpArgAspGly
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                  51 TTAAGGAGTCGACAACAGGTGGGAATGAGATCACGAAATCAAGGTGGAGAAAGTTCATCT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAACTATCAAAAGGCACCTCAAACCATCTGGAGAAAGTGAGAAAAAGATAAQAAGTCT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       680 LeuargSerGludinLysAlaThrGluLysGluArgValAlaGlndluLysAspGln
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                                                                                                                         Sequence 4, Application US/08467781
; Sequence 4, Application US/08467781
; Patent No. 5786156
; GENERAL INFORMATION:
    APPLICANT: TOUKATLY, GARAM P
    TITLE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE TITLE OF INVENTION: INTERIOR NUCLEAR MATRIX
    NUMBER OF SEQUENCES: 6
    CORRESPONDENCE ADDRESS: ADDRESSE: TESTA, HURWITZ & THIBEAULT
    STREET: 125 HIGH STREET
    CITY: BOSTON
    STATE: MA
                                                                                                                                                                                                                          THE
                                                                                                                                                                                                                                                                                                                                               COUNTAIN USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN 1995
FILING DATE: 06-JUN 1995
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-788-793-1 (1-4364) x US-08-467-781-4 (1-2101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 2, 229
REFERENCE/DOCKET NUMBER: MTP-013
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GIARACTERISTICS:
LENGTH: 2101 amino acids
TYPE: amino acid
TYPE: amino acid
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409.50
36.09%
19.51%
5.30%
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2089 IleGly 2090
                                                        3693 CTTGGA 3698
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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                            USA
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Oy 1800 GGTAAACTGAGGAGGGAAGAAGGT  Db 1448AlaGluGluAsnArgG  Qy 1860 AAGAAGCGGCTTGATGGCATAGAGG  Db 1455 GlyGluArgAlaAsnLeuGlyArgGlnP  Qy 1917 TGCAAGGGTCTGAGTTCACC  Db 1475 LygTyrValGlnGluLeuAlaAlaValA	Qy         1968 ACGCTTGAAATCGAGACTGAAGAAAC	Oy 2085 GATAAGGCAAACTTCCTCTCCCAGCAGC	2205 1560 2265	Db 1580 AsnGluLeuGlnAlaGlnLeuSerGlnL, Qy 2325 CAGCAAAGATTTATGGAAGAAACTA ::::: Db 1600 MetGluLysAlaLysThrHisTyrAspA Ov 2385 CTGACCAAGGAGCTAGAGCTTTCCAAGG	1620 2445 1639	2496 1657 2556 1671	Oy 2616 CGGTCCTCGGCTCCTCGACAGGTATCCCC  Db 1690 ThrAspAlaLeuLysSerArgGlubrOG  Qy 2676 TGGATTCCTTGGATGAAAAAGGAAA  Db 1710 SerLeuAspLeuSerCysGluGluG  Qy 2736 AGGCCAAACCAGGGTGCAGGCACC  Db 1729 ArgThrGlnProAspGlyThrSerValP  Qy 2775 CTAGCACAAAGCAGGCCCCCCTAC  Db 1749 L	2835
948	GAGGAGCTGGAAGACCCAATAAAGCCTTCAGAAGGCAGAGGAAGACCTCAGGAGCTG :::        GlnGluLeuGlyHisSerGlnSerAlaLeuAlaSerAlaGlnArgGluLeuAlaAlaPhe AGAGAGAAAATTGCCAAA	ArgThrLysValGlnAspHisSerLysAlaGluAspGluTrpLysAlaGlnValAlaArg       121         GGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGAG       121	1236 IlebeuABnArgGinValLeuGluLyBGluGLyGluSerLyBGluLeuLyBArgLeuVal 1255 1263	1276 GlnProAlaThrValProGluLeuGlnAsnAlaAlaLeuLeuCysGlyArgArgCysArg 1295 1284CGGGAGCTGAAGAAGCTCCAAGAGGAAGAACACCACAGCAAGGAACTT 1334	1335 AGACTAGAAGTGGAGAAGAGGATGTCTGAGCTGGAGAAGCGAGAGGGAGG		1575 AAGTCCTTCACTGTGATGGTGGATGAGGAAAATATGATGGAGAAAATAAGGAA 1634	
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1800	ACTGAGGAGCGAGAAGAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTA 18
1448	145
96	GCGGCTTGATGGCATAGAGGAGGGAGGGAAATAAACCGAGGTAGGTCG 191
45	14
1475	AICAGAGACIA 196 :::    ::: LeuAlaGluVal 149
1968	ACGCTTGAAATCGAGAGCTGAAAACGGCTCCAGCAGTTGGAGGTGGTGGAGGGG 2024
2025	GACTTGATGAAGACCGAGGACGAATATGACCAGTTGGAGCAGAAGTTCAGAACCGAGCAG 2084
80	214
53	154
2145	AAAGCCATAGAGAAAGGGGGGGGGGGGCCAGGAACCGGACTGGGACTACGG 2204
2205	226
1560	AlavalGlnAlaGlnGlyGlyGluSerGlnGlnGluAlaGlnArgPheGlnAlaGlnLeu 1579
2265	CACGAGCTGATGAACAAGGAAGCAGCTGTCTCAGCTCCAAGTCGACTATTCGGTCCTT 2324 :::
2325	CAGCAAAGATTTATGGAAGAAGAACTAAGAACAAGAACATGGGGAGGGA
1600	MetGluLysAlaLysThrHisTyrAspAlaLysLysGlnGlnAsnGlnGluLeuGlnGlu 161
2385	CTGACCAAGGAGCTAGAGCTTTCCAAGCGCTACAGCCGAGCTCTCAGGCCGAGTGGGAAC 2444 :::         :::         GlnLeuArgSerLeuGluGlnLeuGlnLysGluAsnLysGluLeuArgAlaGluAla 1638
2445	o .
1639	
2496	196 GCGGTGTGCGGGGGATGCTGCGGAGGAGGAGGCCCCGGCTGTGTTCGTTC
2556	CAGGAGGAAATCACATCATGAGTAATCTTCGACAGGTAGGCCTGAAGAAACCCATGGAA 261
	AlaGlnValAlaHisAlaAspGlnGlnLeuArgAspLeuGlyLysPheGlnValAla 168
2616	CGGTCCTCGGTCCTCGACAGGTATCCCCCAGCGAATGAGGTCACCATGAGGAAGTCT 2675 ::::::
2676	273
1710	7/7
2736 1729	AGGCCAAACCAGGGTGCAGGGCACCCGGGGAGCTGGTC
2775	6 1
1749	LeuProProLysValGluSerLeuGluSerLeuTyrPheThrFrolleProAlaArgSer 1768 armgrcaccrngaangarracaagacccacacargcaagagarrarrc2879
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1769 GlnAlaProLeuGluSerSerLeuAspSerLeuGlyAspValPheLeuAspSerGlyArg 1788
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                                                         CCAAGAATAACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCAAAAGTGCAGAT 2978
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1809 LeuAspValGluGluProAspSerAlaAsnSerSerPheTyrSerThrArgSerAlaPro 1828
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1829 AlaSerGlnAlaSerLeuArgAlaThrSer-----SerThrGlnSerLeuAlaArgLeu 1846
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1957 GlnProileGlnIle---AlaGlu------GlyThrGlyIleThrThrArgGlnGln 1972
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|1973 ArgLysArgValSerLeuGluProHisGlnGlyProGlyThrProGluSerLysLysAla 1992
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                                                                                                                                                                                                                             1847 GlySerProAspTyrGlyAsnSerAlaLeuLeuSerLeuProGlyTyrArgPro----- 1864
                                                                                                                                                                                                                                                       3096 ATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAG 3155
                                                                                                                                                                                                                                                                                                         -----CACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGGCCTGCCGCTGAAGGC 3326
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Sequence 4, Application US/08195487

Patent No. 5783403

GENERAL INFORMATION:
APPLICANT: LIDGARD, GRAHW
ITILE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
ITILE OF INVENTION: NOVEL MALIGNANT CELL TYPE MARKERS OF THE
ITILE OF INVENTION: INTERIOR NUCLEAR MATRIX
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STATE STREET
STREET: SA STATE STREET
STATE: MA.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,487
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER: US/07/901,701
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: MTP-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEPHONE: 617/248-7100
TELEPHONE: 210/248-7100
TELEPHONE: 210/248-7100
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	777			y 405 b 817	у 444	b 837	у 486	b 857			y 516 b 897	у 567							716 d			705	1017	y 765 b 1037			у 873	b 1077	у 933	b 1096	-	

1916	1860 AAGAAGCGGTTGATGGCATAGAGGAGGTAGAAAGGGAAATAAACCGAGGTAGGT	1. 1. 14
1859	GGTAAACTGAGGAGCGAAGAAGAAAGGTCCTGTGAACTGAGCTGCAGTGTAGACTTACTA	14
1799	1746 TCTGAAATGGAGGAAAAGGAGTACAGTCTGACAAAGGAGGAGGGATGAGCTGATG 1 :::         :::         :::         :::         :::           :::           :::           :::           :::             :::             :::	ਜ਼ ,ਜ ਜ਼ ,ਜ
1745	1686 AAAGTCATGGATGACGGAAAAGCTAATCGAGGAAAGCAAGAAGCTTTTAAAACTCAAA 1 1:::::::::::::::::::::::::::::::::	ř ř.
1685	1635 GAAGAGGAAAGTGGATGGGTTGAATAAAAACTTTAAGGTGGAGCAGGGA 1 	1 1
1387	:::::::     1382ArgGluGluLeuGluGluGluGluGluGlu	Ħ
1634	1575 AAGTCCTTCACTGTGATGCTGGTGGATGAGAGAAAAATATGATGGAGAAAATAAAGCAA 1	16
1574	1515 TGCTCCGAGAGTAGACTGGAGAGAGCCGAGTTAAGCCTCAAAGATGACCTTACAAAGCTG 1 	11 11
1371	:::    :::        52 SerThrGlnAlaLeuValSerGluLeuLeuProAlaLy8HisLeuCysGlnGlnLeuGln	13
1514	S CTAACCAAAGACCTGCTGAACGAGCTGGAGGTCAAGAGTCGAGTTAAAGAACTCGAA	14
1454	95 TTCAGCCGGAGTAAGTCGGAATGCACCCGGCTCCATCTGAACCTGGAGAAGGAGAAGAAC	133
1394	1335 AGACTAGAAGTGGAGAAGCTGCAGAAGAGGATGTCTGAGCTGGAGAAGCG 1 	ដ ដ
1334	1284CGGGAGCTGAAGAAGAAGCTCCAAGAGAACACACACAGCAAGGAACTT	12
1295	1276 GlnProAlaThrValProGluLeuGlnAsnAlaAlaLeuLeuCysGlyArgArgCysArg	12
1283	1283	11
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1262	1215 AGTCTGCGCAAGCGCGTGCTTGAGATGGAGGCAAGGATGAAGAGATC 1 	12.
1214	1176 GGGGAATGTGGAAACTCCAGTCTCATGGCGGAAGTGGG 3 	H H
1175	1158 AGAGAGAAAATTGCCAAA 1177 	ਜ ਜੋ
1157 1195	3 GAGGAGCTGGAAGACCAATAAAAGCCTTCAGAAGGCAGAGGAAGAAGCTCGGGAGCTG :::	គ គ
1175	1156 SerArgAlaGluArgAspSerAlaLeuGluThrLeuGlnGlyGlnLeuGluGluThsala	i ii
1155	s CysGlnLysGlnGlnGluGlnAlaAspSerLeuGluArgSerLeuGluAlaGluArgAla	H

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TGCCCGGAA ArgAlaAspAla ArgAlaAspAla AcGGCTCCAGCAG    :::     :::  GluLeuGluVal GACCACTTGGAGArg CTCGAGGAAATC       :::	TAGAGAGGGAGGCGGTGAGCCGGAAGCGGAAGCGAAGCG	GCCTCCACTGGG GlnGlnalaGly GAGACCCCGGCTA GLALAGASPLEUW CCACCACACATA GlnAlaLysProleuw GlyThrProleuw GlyThrProleuw GlyThrProleuw HIIIIII SerLeurysPhen ACATCCGTGTG SerLeurysPhen SerLeurysPhen SerLeurysPhen SerLeurysPhen HOGGGGGGGGGTGG SerLeurysPhen SerLeurysPhen HOGGGGGGGGTGG SerLeurysPhen HOGGGGGGGGTGG SerLeurysPhen SerLeurysPhen HOGGGGGGGGTGG HOGGGGGGGGTGG HOGGGGGGGGTGG HOGGGGGGGGGG
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1917 TG 1475 Ly 1968 AC 1495 G1 2025 GA 2085 GA		2445 GGC 1639 2496 GCC 1657 Gln 2556 CAG 1671 Ala 2616 CGG 1710 Ser 2775 TA 2775 CTA 2775 CTA 2775 CTA 2775 GTA 2775

1864 1880 GlyAlaProProGlyArgAsnSerPheTyrMet---GlyThrCysGlnAspGluProGlu 1898 2919 CCAAGAATAACCATTATTCCATCACCCAATGTCATGTCGCAAAAGCCCAAAAGTGCAGAT 2978 2979 CCTACTCTCGGCCCAGAACGAGCCATGTCCCCTGTCACGATTACTACTATTTCCAGAGAG 3038 3039 AAGAGCCCGGAAGGTGGAAGGAGCGCCTTTGCCGACAGGCCTGCA---TCCCCCCATCCAA 3095 3096 ATCATGACGGTGTCAACATCTGCAGCTCCCACTGAAATCGCTGTCTCTCCTGAATCTCAG 3155 3216 CCCGTGCGGAAGTACAACTCCAATGCTAATATCATCACCACGGAAGACAATAAAATT--- 3272 3273 -----CACATTCACCTGGGTTCTCAGTTTAAGCGATCTCCTGGGCCTGCCGCTGAAGGC 3326 :::::: 1937 IleThrAspGluGluMetLysThrGlyAspProGlnGluThrLeuArgArgAlaSerMet 1956 |||::: ::: |||||| 1957 GlnProlleGlnIle---AlaGlu------GlyThrGlyIleThrThrArgGlnGln 1972 3327 GTGAGC----- 3350 3351 ---CCTGTCAACGTGACAGCGGAGAGGAGGTTTCTACAGGCACAGTCCTTCGCTCTCCC 3407 3408 AGGAACCACTCTCT-------TGAGACCCGGTGCTAGCAAAGTG ||| 1973 ArgLysArgValSerLeuGluProHisGlnGlyProGlyThrProGluSerLysLysAla 1992 3447 ACCAGCACTATA-----GTC 3473 1993 ThrserCysPheProArgProMetThrProArgAspArgHisGluGlyArgLysGlnSer 2012 3474 ACAACGTCATCCACACGAGGAACCCAATCAGTGTCAGGACAAGATGGGTCATCTCAGCGG 3533 2013 ThrThrGluAlaGlnLysLysAlaAlaProAlaSerThrLysGlnAlaAspArgArgGln 2032 3534 CCT-------ACCCCCACCGCATTCCTATGTCAAAGGTATGAAA 3572 2033 SerMetAlaPheSerIleLeuAsnThrProLysLysLeuGlyAsnSerLeu---LeuArg 2051 3573 GCTGGAAAGCCAGTAGTGGCAGCCTCAGGAGCAGGAAATCTGACCAAATTCCAGCCTCGA 3632 2052 ArgGlyAlaSerLysLysAlaLeuSerLysAlaSerProAsnThrArgSerGlyThrArg 2071 2072 ------ArgSerProArgIleAlaThrThrThrAlaSerAlaAlaThaAlaAla 2088 |||||||::: ||| |||||| 1847 GlySerProAspTyrGlyAsnSerAlaLeuLeuSerLeuProGlyTyrArgPro-----3693 CTTGGA 3698 ŏ g ò g ò 8 8 8 8 Д à ŏ qq 8 8 8 В ò g

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Search completed: September 7, 2004, 14:12:00 Job time : 353.5 secs